

50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala
 225

<210> 237
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> RXC02238

<400> 237

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ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 90 95

cac 408

<210> 238

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
 1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
 20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
 35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
 50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
 65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 85 90 95

<210> 239

<211> 1827

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXC00128

<400> 239

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
 Val Ser Lys Ile Ser
 1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg	163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val	
10 15 20	
gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc	211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg	
25 30 35	
tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg	259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro	
40 45 50	
aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg	307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala	
55 60 65	
tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg	355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly	
70 75 80 85	
acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc	403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg	
90 95 100	
att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att	451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile	
105 110 115	
gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt	643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe	
170 175 180	
gat cct tct ggc cag gtg ttg gtg ggg gat ccg cgt tgg ttg ttc aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg	883

Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
 250 255 260
 tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931
 Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
 265 270 275
 gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979
 Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
 280 285 290
 ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg
 1027
 Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
 295 300 305
 ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg
 1075
 Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
 310 315 320 325
 agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg
 1123
 Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
 330 335 340
 att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac
 1171
 Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
 345 350 355
 gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg
 1219
 Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
 360 365 370
 ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt
 1267
 Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
 375 380 385
 ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga
 1315
 Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
 390 395 400 405
 tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg
 1363
 Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
 410 415 420
 cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act
 1411
 Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
 425 430 435
 ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc
 1459
 Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
 440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag
1507

Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca
1555

Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg
1603

Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat
1651

Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac
1699

Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat
1747

Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg
1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc
1827

Val Ala Tyr

<210> 240

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
 85 90 95
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
 530 535 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
 545 550 555 560

Arg Ala Ala Pro Val Val Ala Tyr
 565

<210> 241
 <211> 1344
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1321)
 <223> ~~BYA02240~~

<400> 241
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 aagactattt attctcaact tcttcgaaag aagggtattt gtg gct cag cca acc 115
 Val Ala Gln Pro Thr
 1 5

gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
 10 15 20

aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211
 Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu
 25 30 35

aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259
 Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly

40	45	50	
atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile 55 60 65			307
cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser 70 75 80 85			355
gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly 90 95 100			403
gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala 105 110 115			451
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp 120 125 130			499
cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met 135 140 145			547
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln 150 155 160 165			595
gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr 170 175 180			643
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp 185 190 195			691
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp 200 205 210			739
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp 215 220 225			787
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn 230 235 240 245			835
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu 250 255 260			883
acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His 265 270 275			931
ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser 280 285 290			979

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc
1027

Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
295 300 305

ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca
1075

Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
310 315 320 325

aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc
1123

Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly
330 335 340

ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg
1171

Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu
345 350 355

cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac
1219

Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
360 365 370

gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt
1267

Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu
375 380 385

cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag
1315

Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys
390 395 400 405

ttg gcc taaaaatctg atgtagtatc ttc
1344

Leu Ala

<210> 242

<211> 407

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 242

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr
1 5 10 15

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu
20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr
35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser
50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile

65		70		75		80
Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val						
	85		90		95	
Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp						
	100		105		110	
Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg						
	115		120		125	
Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu						
	130		135		140	
Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser						
	145		150		155	
Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg						
	165		170		175	
Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg						
	180		185		190	
Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu						
	195		200		205	
Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp						
	210		215		220	
Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile						
	225		230		235	
Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met						
	245		250		255	
Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly						
	260		265		270	
Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser						
	275		280		285	
Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn						
	290		295		300	
Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr						
	305		310		315	
Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp						
	325		330		335	
Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu						
	340		345		350	
Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu						
	355		360		365	
Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg						
	370		375		380	
Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu						
	385		390		395	
					400	

Arg Ala Ala Leu Lys Leu Ala
405

<210> 243
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXA00780

<400> 243
cctttttaagt ccttctttgc ccgtgaataa ttctctggat agtttccacg tgcagttaag 60
tcacgctggt agacttgcct gcatgctctc gacaataaaa atg atc cgt gaa gat 115
Met Ile Arg Glu Asp
1 5
ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu
10 15 20
aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val
25 30 35
gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu
40 45 50
gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala
55 60 65
acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile
70 75 80 85
~~ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403~~
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val
90 95 100
acc ctc ggc gga cag gtt ctc acc caa acc aag cgc cac ccc acg ctc 451
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu
105 110 115
tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile
120 125 130
acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys
135 140 145
gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg
150 155 160 165

cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643
 Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr
 170 175 180

att taagaacagt tagcgcccta cct 669
 Ile

<210> 244

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met Ile Arg Glu Asp Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala
 1 5 10 15

Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile
 20 25 30

Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly
 35 40 45

Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu
 50 55 60

Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly
 65 70 75 80

Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met
 85 90 95

Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys
 100 105 110

Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys
 115 120 125

Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn
 130 135 140

Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile
 145 150 155 160

Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val
 165 170 175

Asp Pro Asp Tyr Tyr Ile
 180

<210> 245

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA00779

<400> 245

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caacaaaaac agcacttcaa tgattggagc accacccgac atg ggc aat gtg tac 115
                                         Met Gly Asn Val Tyr
                                         1 5
aac aac atc acc gaa acc atc ggc cac acc cca ctg gta aag ctg aac 163
Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro Leu Val Lys Leu Asn
          10          15          20
aag ctc acc gaa ggc ctc gac gca act gtc ctg gtc aag ctt gag tca 211
Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu Val Lys Leu Glu Ser
          25          30          35
ttc aac cca gca aac tcc gtc aag gac cgt atc ggt ctg gcc atc gtt 259
Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile Gly Leu Ala Ile Val
          40          45          50
gaa gat gca gag aag tcc ggt gca ctg aag cca ggc ggc acc atc gtt 307
Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro Gly Gly Thr Ile Val
          55          60          65
gaa gca acc tcc ggc aac acc ggt atc gca ctg gca atg gtc ggc gct 355
Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu Ala Met Val Gly Ala
          70          75          80          85
gca cgc gga tac aac gtt gtt ctc acc atg ccg gag acc atg tcc aac 403
Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro Glu Thr Met Ser Asn
          90          95          100
gag cgt cgc gtt ctc ctc cgc gct tac ggt gca gag atc gtt ctt acc 451
Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala Glu Ile Val Leu Thr
          105          110          115
cca ggt gca gca ggc atg cag ggt gca aag gac aag gca gac gaa atc 499
Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp Lys Ala Asp Glu Ile
          120          125          130
gtc gct gaa cgc gaa aac gca gtc ctt gct cgc cag ttc gag aac gag 547
Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg Gln Phe Glu Asn Glu
          135          140          145
gca aac cca cgc gtc aac cgc gac acc acc gcg aag gaa atc ctc gaa 595
Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala Lys Glu Ile Leu Glu
          150          155          160          165
gac acc gac ggc acc gtt gat atc ttc gtt gca agc ttc ggc acc ggc 643
Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala Ser Phe Gly Thr Gly
          170          175          180
gga acc gtc acc ggc gtt ggc cag gtc ctg aag gaa aac aac gca gac 691
Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys Glu Asn Asn Ala Asp
          185          190          195
gta cag gtc tac acc gtc gag cca gaa gcg tcc cca ctt ctg acc gct 739
Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser Pro Leu Leu Thr Ala
          200          205          210

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ggc aag gct ggt cca cac aag atc cag ggc atc ggc gca aac ttc atc 787
 Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile Gly Ala Asn Phe Ile
 215 220 225

ccc gag gtc ctg gac cgc aag gtt ctc gac gac gtg ctg acc gtc tcc 835
 Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp Val Leu Thr Val Ser
 230 235 240 245

aac gaa gac gca atc gca ttc tcc cgc aag ctc gct acc gaa gag ggc 883
 Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu Ala Thr Glu Glu Gly
 250 255 260

atc ctc ggc ggt atc tcc acc ggc gca aac atc aag gca gct ctt gac 931
 Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile Lys Ala Ala Leu Asp
 265 270 275

ctt gca gca aag cca gag aac gct ggc aaa acc atc gtc acc gtt gtc 979
 Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr Ile Val Thr Val Val
 280 285 290

acc gac ttc ggc gag cgc tac gtc tcc acc gtt ctt tac gaa gac atc
 1027
 Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val Leu Tyr Glu Asp Ile
 295 300 305

cgc gac taattcttag cgactgttaa cca
 1056
 Arg Asp
 310

<210> 246
 <211> 311
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 246
 Met Gly Asn Val Tyr Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro
 1 5 10 15

Leu Val Lys Leu Asn Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu
 20 25 30

Val Lys Leu Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
 35 40 45

Gly Leu Ala Ile Val Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro
 50 55 60

Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
 65 70 75 80

Ala Met Val Gly Ala Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro
 85 90 95

Glu Thr Met Ser Asn Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala
 100 105 110

Glu Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp
 115 120 125

Lys Ala Asp Glu Ile Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg
 130 135 140
 Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala
 145 150 155 160
 Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala
 165 170 175
 Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys
 180 185 190
 Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser
 195 200 205
 Pro Leu Leu Thr Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile
 210 215 220
 Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp
 225 230 235 240
 Val Leu Thr Val Ser Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu
 245 250 255
 Ala Thr Glu Glu Gly Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile
 260 265 270
 Lys Ala Ala Leu Asp Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr
 275 280 285
 Ile Val Thr Val Val Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val
 290 295 300
 Leu Tyr Glu Asp Ile Arg Asp
 305 310

<210> 247

<211> 623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(600)

<223> RXN00402

<400> 247

act gac gaa aag gat gga aag cca gta ttg ccc tac ttc gtc act cca 48
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15

gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
 20 25 30

ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc 144
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
 35 40 45

ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt 192

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<210> 248
<211> 200
<212> PRT
<213> Corvnebacterium glutamicum
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<400> 248
Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
  1                      5                      10                      15
Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
      20                      25                      30
Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
      35                      40                      45
Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
      50                      55                      60
Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
      65                      70                      75                      80

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<210> 249
<211> 599
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(576)  
<223> FRXA00402
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<400> 249																	
gta	ttg	ccc	tac	ttc	gtc	act	cca	gat	gct	gct	tac	cac	gga	ttg	aag	48	
Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys		
1				5					10					15			
tac	gca	gac	ctt	ggt	gca	cca	gcc	ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	96	
Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu	Lys	Val	Arg	Val	Gly		
			20					25					30				

ctt	cta	cgc	gac	acc	ggc	tcc	acc	ctc	tcc	gca	ttc	aac	gca	tggt	gct	144
Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	
		35					40					45				
gca	gtc	cag	ggc	atc	gac	acc	ctt	tcc	ctg	cgc	ctg	gag	cgc	cac	aac	192
Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	
		50				55					60					
gaa	aac	gcc	atc	aag	gtt	gca	gaa	ttc	ctc	aac	aac	cac	gag	aag	gtg	240
Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	Asn	Asn	His	Glu	Lys	Val	
		65			70					75					80	
gaa	aag	gtt	aac	ttc	gca	ggc	ctg	aag	gat	tcc	cct	tggt	tac	gca	acc	288
Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	
				85					90					95		
aag	gaa	aag	ctt	ggc	ctg	aag	tac	acc	ggc	tcc	gtt	ctc	acc	ttc	gag	336

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110
 atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125
 cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140
 cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160
 cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528
 Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
 165 170 175
 acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576
 Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
 180 185 190
 tagctttaaa tagactcacc cca 599

<210> 250

<211> 192

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 250

Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
 1 5 10 15

Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30

Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45

Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60

Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
 65 70 75 80

Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110

Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125

Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140

His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160

Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
165 170 175

Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
180 185 190

<210> 251

<211> 613

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(613)

<223> RXS00405

<400> 251

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ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac 115
Met Pro Lys Tyr Asp
1 5

aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca 163
Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala
10 15 20

ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac 211
Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr
25 30 35

caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt 259
Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg
40 45 50

ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca 307
Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro
55 60 65

acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc 355
Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val
70 75 80 85

cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att 403
His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile
90 95 100

ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc 451
Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu
105 110 115

tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt 499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly
120 125 130

atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag 547

Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln
 135 140 145

gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595
 Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala
 150 155 160 165

aac cca cag gca gac gtc 613
 Asn Pro Gln Ala Asp Val
 170

<210> 252

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
 1 5 10 15

Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
 20 25 30

Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
 35 40 45

His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
 50 55 60

Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
 65 70 75 80

Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
 85 90 95

Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
 100 105 110

Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
 115 120 125

Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
 130 135 140

Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
 145 150 155 160

Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
 165 170

<210> 253

<211> 1812

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1789)

<223> RXC00164

ctactttgcg qqaggttatg aaatgagtgg ggagacgtcg aaaagcatgc gctttccggt 60

cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163
Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly
10 15 20

gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211
Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu Gly Arg Ile Val Asp
25 30 35

ctg gtg tcc gat ggc gcg cag atg cgt gat ttt gtt gag ctc agt gtg 259
Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe Val Glu Leu Ser Val
40 45 50

att ctc att gcg gtg gca att gcc ggc gcg gtg ctc agt gcg tgc ggg 307
Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val Leu Ser Ala Cys Gly
55 60 65

ttc	tat	gtg	gtg	tcg	cgg	att	tct	gag	aag	att	atc	gcc	aat	ttg	agg	355
Phe	Tyr	Val	Val	Ser	Arg	Ile	Ser	Glu	Lys	Ile	Ile	Ala	Asn	Leu	Arg	
70					75					80					85	

gaa gat atg gtg ggc acc gcg ctt ggg ttg ccc acg cac cag gtg gaa 403
Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro Thr His Gln Val Glu
90 95 100

gat gcg ggc tct ggc gat ttg gtg agc cgc tcc acc gat gat gtc tcc 451
Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser Thr Asp Asp Val Ser
105 110 115

gag cta tcc gca gcg gtg aca gag acc gtc ccg att tta agt tcc tca 499
Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro Ile Leu Ser Ser Ser
120 125 130

ctg ttt acc att gcc gcg acg atc att gcg ctg ttt tct ttg gac tgg 547
Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu Phe Ser Leu Asp Trp
135 140 145

caa ttt gtg ctc att cct gtc gtg gtg gcg ccg gtg tac tac ttc gcg 595
Gln Phe Val Leu Ile Pro Val Val Val Ala Pro Val Tyr Tyr Phe Ala
150 155 160 165

tcc aag cac tat ttg agc aag gcg ccg gat cgg tat gcg gca gaa cgc 643
Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg Tyr Ala Ala Glu Arg
170 175 180

gcg gcg atg gcg gag cgt gcg cga aag gta ctt gag gct att cgc ggg 691
Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu Glu Ala Ile Arg Gly
185 190 195

cgt gca act gtg cgg gcg tat tcc atg gaa gat gcc atg cat aat cag 739
Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp Ala Met His Asn Gln
200 205 210

att gat cag gcg tcg tgg tct gtg gtg gtc aag ggt att cgt gcg cgc 787

Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys Gly Ile Arg Ala Arg
 215 220 225
 acc acc atg ttg att ttg aac atg tgg atg ctg ttt gcg gaa ttc ctc 835
 Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu Phe Ala Glu Phe Leu
 230 235 240 245
 atg ctc gcg gtc gcg ttg gtg atc ggc tac aag ctg gtc att gat aat 883
 Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys Leu Val Ile Asp Asn
 250 255 260
 gcg ctg acg atc ggc gcg gtt acc ggt gcc gtg ctg atg att att cgt 931
 Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val Leu Met Ile Ile Arg
 265 270 275
 ctg cgt ggc ccg atg aat atg ttc atg cgc gtg ctc gac acc att caa 979
 Leu Arg Gly Pro Met Asn Met Phe Met Arg Val Leu Asp Thr Ile Gln
 280 285 290
 tcc ggc tat gcg tcg ctg gcg cgc atc gtg gga gtt gtt gcg gat ccg
 1027
 Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly Val Val Ala Asp Pro
 295 300 305
 ccg att cct gtg ccc gac agc ggt gtg aaa gca cct cag ggc aaa gtg
 1075
 Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala Pro Gln Gly Lys Val
 310 315 320 325
 gaa ttg cgc aac gtc agc ttt agc tat ggc gat tcc tgg gcg gtg aaa
 1123
 Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp Ser Trp Ala Val Lys
 330 335 340
 gac atc gac atc acg atc aat tcc ggc gaa act gtc gcg ctc gtg ggc
 1171
 Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr Val Ala Leu Val Gly
 345 350 355
 gca tct ggc gca ggt aag acg acg gtc gcc gcc ttg ctg gcg ggc ttg
 1219
 Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala Leu Leu Ala Gly Leu
 360 365 370
 cgg gtg cca gat caa ggg caa gtg ctt gtc gac gac ttc ccc gtc tct
 1267
 Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp Asp Phe Pro Val Ser
 375 380 385
 cac ctc tct gac cgc gag cgt atc gcc cgc ttg gcc atg gtc agc cag
 1315
 His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu Ala Met Val Ser Gln
 390 395 400 405
 gag gtt cat gtt ttc tcc ggc acg ctg cgc cag gat ctc acc ttg gct
 1363
 Glu Val His Val Phe Ser Gly Thr Leu Arg Gln Asp Leu Thr Leu Ala
 410 415 420
 aaa cca gat gcc tcc gat gag gaa tta gcg cat gct ctt ggg caa gtt
 1411

Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His Ala Leu Gly Gln Val
 425 430 435

aat gcc ctt gac tgg ttg gag agt ctt cca gaa gga ctg gac acg gtc
 1459

Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu Gly Leu Asp Thr Val
 440 445 450

gtt ggt gcg cga gga atc cag cta gaa cca gtg gtg gct cag cag ttg
 1507

Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu
 455 460 465

gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat
 1555

Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala Ile Val Ile Met Asp
 470 475 480 485

gaa gcc acg gca gaa gca gga tcg gcg ggt gcc agc gca ctg gaa gag
 1603

Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu
 490 495 500

gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac
 1651

Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His
 505 510 515

cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag
 1699

Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys
 520 525 530

ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg
 1747

Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly
 535 540 545

ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga
 1789

Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg
 550 555 560

tagttgactg ttcaatgcgt tga
 1812

<210> 254

<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Val Gly Arg Ile Pro Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val
 1 5 10 15

Leu Leu Ser Ala Gly Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu
 20 25 30

Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe
 35 40 45

Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val
 50 55 60
 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile
 65 70 75 80
 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro
 85 90 95
 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser
 100 105 110
 Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro
 115 120 125
 Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu
 130 135 140
 Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro
 145 150 155 160
 Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg
 165 170 175
 Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu
 180 185 190
 Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp
 195 200 205
 Ala Met His Asn Gln Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys
 210 215 220
 Gly Ile Arg Ala Arg Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu
 225 230 235 240
 Phe Ala Glu Phe Leu Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys
 245 250 255
 Leu Val Ile Asp Asn Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val
 260 265 270
 Leu Met Ile Ile Arg Leu Arg Gly Pro Met Asn Met Phe Met Arg Val
 275 280 285
 Leu Asp Thr Ile Gln Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly
 290 295 300
 Val Val Ala Asp Pro Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala
 305 310 315 320
 Pro Gln Gly Lys Val Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp
 325 330 335
 Ser Trp Ala Val Lys Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr
 340 345 350
 Val Ala Leu Val Gly Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala
 355 360 365

Leu Leu Ala Gly Leu Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp
370 375 380

Asp Phe Pro Val Ser His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu
385 390 395 400

Ala Met Val Ser Gln Glu Val His Val Phe Ser Gly Thr Leu Arg Gln
405 410 415

Asp Leu Thr Leu Ala Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His
420 425 430

Ala Leu Gly Gln Val Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu
435 440 445

Gly Leu Asp Thr Val Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val
450 455 460

Val Ala Gln Gln Leu Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala
465 470 475 480

Ile Val Ile Met Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala
485 490 495

Ser Ala Leu Glu Glu Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala
500 505 510

Leu Val Val Ala His Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile
515 520 525

Leu Val Met Asp Lys Gly Glu Val Val Glu Ser Gly Thr His Gln Glu
530 535 540

Leu Leu Asp His Gly Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser
545 550 555 560

Val Gly Arg

<210> 255

<211> 1713

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1690)

<223> RXC01191

<400> 255

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cggtgttggtg gccgtgcgcg ggttggttagg gccctgggcg gtg ggt gga ctc gtc 115
Val Gly Gly Leu Val
1 5

gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163
Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala
10 15 20

ctg ctt atc gtg gct ggc ggc gtt gtt tgc agc ctg ggc acg tgg tgg	211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp	
25 30 35	
ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg	259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu	
40 45 50	
cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att	307
Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu Asp Ala Asn Thr Ile	
55 60 65	
gaa acg gcg ggg cgc ggc gac gtg att tgc cgt atc gcg gat gat tgc	355
Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser	
70 75 80 85	
cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag	403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln	
90 95 100	
gcg ggc ttt acc gtg gtg att tcc gcg ttt ggc atg gcg gcg gtt gat	451
Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp	
105 110 115	
tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc	499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr	
120 125 130	
acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag	547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu	
135 140 145	
cgc gag gcc ttt ggg gtg cgc acg cag ccg ctt gtc ggc gca gtc gaa	595
Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu Val Gly Ala Val Glu	
150 155 160 165	
ggc gcg gaa acc ttg cgc gct ttc cgc gca gaa gat aca gaa tta aag	643
Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
170 175 180	
cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
200 205 210	
atc acc ctc gtg ctc atc ttg ggc acc ggc ttt tac ctg gtc aac atc	787
Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
gat ctg gtc acc gtc ggc gca gtc tca acc gcc gca ctg atc ttc cac	835
Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
250 255 260	
caa tcc gcc agc gca tgc ctg atc cgc atg gtg ggc gtt att aac gcg	931

Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val Gly Val Ile Asn Ala
 265 270 275

gca tcg aac cag gtc agc ggc acc tcg ccg gcg tct gcc agc acc gct 979
 Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala Ser Ala Ser Thr Ala
 280 285 290

tta acg ctt ttc gac gtc tcc cac cac tat cac act gca ccc gtc atc
 1027
 Leu Thr Leu Phe Asp Val Ser His His Tyr His Thr Ala Pro Val Ile
 295 300 305

aag aat gca tcc gtg cag ctg gaa cca ggg gaa cac atc gcc att gtg
 1075
 Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val
 310 315 320 325

ggt gcg acc ggc gct ggt aaa agc acg ctc gcc ctc att gcg gca ggc
 1123
 Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala Leu Ile Ala Ala Gly
 330 335 340

ctg ctc agc cca act tcc ggg cag gtg gct ctc ggc gga tcg agt ttt
 1171
 Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu Gly Gly Ser Ser Phe
 345 350 355

tct aac gtc gaa ccg gaa gca ttg cgc cag aag atc gcg atg gtc agc
 1219
 Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser
 360 365 370

caa gaa atc cac tgc ttc cga gga tct gtt tta gat aat ctt cgt atc
 1267
 Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile
 375 380 385

gca cgc ccc gaa gcc acc gat gcg gac atc cac gcc gtt ctc gcc gat
 1315
 Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp
 390 395 400 405

att ggt gat tcc tgg ttg gag cgc tta ccg caa ggc ata gac acc atc
 1363
 Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile
 410 415 420

gtg ggt gat ggc gct ttc cgt tta acc tct gtg gaa aac cag atc atg
 1411
 Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met
 425 430 435

gcg ctt gct cgc gta cat ttg gcc gac cta gca atc gtc atc ctt gat
 1459
 Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp
 440 445 450

gaa gca acg gct gaa tca ggc tct gat cat gca aaa cag ctt gaa gat
 1507
 Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp
 455 460 465

gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac
1555

Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His
470 475 480 485

cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc
1603

Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser
490 495 500

gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc gcc
1651

Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly
505 510 515

ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca
1700

Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg
520 525 530

ccaagacca cgc
1713

<210> 256

<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

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20 25 30

Leu Gly Thr Trp Trp Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro
35 40 45

Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu
50 55 60

Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg
65 70 75 80

Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val
85 90 95

Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly
100 105 110

Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile
115 120 125

Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro
130 135 140

Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu
145 150 155 160

Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu
 165 170 175
 Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp
 180 185 190
 Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn
 195 200 205
 Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe
 210 215 220
 Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala
 225 230 235 240
 Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly
 245 250 255
 Met Phe Ser Asp Ile Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val
 260 265 270
 Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala
 275 280 285
 Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His His Tyr His
 290 295 300
 Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu
 305 310 315 320
 His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala
 325 330 335
 Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu
 340 345 350
 Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys
 355 360 365
 Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu
 370 375 380
 Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His
 385 390 395 400
 Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln
 405 410 415
 Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val
 420 425 430
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala
 435 440 445
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala
 450 455 460
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala
 465 470 475 480
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile

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                                485                490                495
Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu
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Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser
      515                520                525

Ala Arg
      530

<210> 257
<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1369)
<223> RXA02646

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catgagtgaa acatacgtgt ctgagaaaag tccaggagtg atg gct agc gga gcg 115
                                Met Ala Ser Gly Ala
                                1                5

gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc 163
Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser
                        10                15                20

tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag 211
Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu
                        25                30                35

gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt 259
Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val
                        40                45                50

cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc 307
Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr
                        55                60                65

caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat 355
Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His
                        70                75                80                85

gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga cgc 403
Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg
                        90                95                100

atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg 451
Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met
                        105                110                115

gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc 499
Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe
                        120                125                130

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gac gaa gca tcg gct gca gcg cat gaa gat gca gag cgc acc ggc gca 547
 Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala
 135 140 145

acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc 595
 Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly
 150 155 160 165

acc gtg gct gct gag atc ttg tcg cag ctg act tcc atg ggc aag agt 643
 Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser
 170 175 180

gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt 691
 Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly
 185 190 195

gtg gtc agc tac atg gct gat atg gca cct cgc act gcg atc gtt ggt 739
 Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly
 200 205 210

atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt 787
 Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly
 215 220 225

gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca 835
 Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala
 230 235 240 245

gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag 883
 Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln
 250 255 260

ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag 931
 Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu
 265 270 275

atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc 979
 Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly
 280 285 290

gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct
 1027
 Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser
 295 300 305

gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat
 1075
 Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr
 310 315 320 325

gcg gaa atc gct gag cgc tcc ttg gtg cgc cgc ggt tta aag cac tac
 1123
 Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr
 330 335 340

ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg
 1171
 Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu
 345 350 355

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc
 1219
 Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu
 360 365 370
 aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg
 1267
 Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu
 375 380 385
 agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg
 1315
 Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser
 390 395 400 405
 gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac
 1363
 Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr
 410 415 420
 ttg acc taaacatagc tgaaggccac ctc
 1392
 Leu Thr

<210> 258
 <211> 423
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 258
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 Gln Ala Arg Ile Ser Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys
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 Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu
 35 40 45
 Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser
 50 55 60
 Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala
 65 70 75 80
 Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu
 85 90 95
 Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys
 100 105 110
 Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val
 115 120 125
 Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala
 130 135 140
 Glu Arg Thr Gly Ala Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr
 145 150 155 160

Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr
 165 170 175

Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly
 180 185 190

Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg
 195 200 205

Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala
 210 215 220

Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe
 225 230 235 240

Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile
 245 250 255

Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly
 260 265 270

Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile
 275 280 285

Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser
 290 295 300

Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn
 305 310 315 320

Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg
 325 330 335

Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln
 340 345 350

Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr
 355 360 365

Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu
 370 375 380

Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu
 385 390 395 400

Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr
 405 410 415

Pro Glu Tyr Glu Tyr Leu Thr
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<210> 259
 <211> 966
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(943)

<223> RXA00766

<400> 259

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ctacggcggg tccatccggc aacaaaaacc caacctacca atg gtt ttt tgg gac 115
Met Val Phe Trp Asp
1 5

gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc 163
Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile
10 15 20

cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa 211
Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys
25 30 35

gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg 259
Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp
40 45 50

gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac 307
Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn
55 60 65

gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc 355
Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser
70 75 80 85

acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac 403
Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp
90 95 100

aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga 451
Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg
105 110 115

gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga 499
Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg
120 125 130

ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc 547
Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val
135 140 145

ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac 595
Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr
150 155 160 165

gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc 643
Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg
170 175 180

gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa 691
Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys
185 190 195

atc cgc acc cct tca ccc ggt ggc gac att ctc ccc gga acc acc caa 739
Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu Pro Gly Thr Thr Gln
200 205 210

gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787
 Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu
 215 220 225

aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835
 Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp Ser Val Trp Leu
 230 235 240 245

gtg tcc tcc gtc cgc gga cca gtt cgg gtg acc agg ctc gat gga cac 883
 Val Ser Ser Val Arg Gly Pro Val Arg Val Thr Arg Leu Asp Gly His
 250 255 260

aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931
 Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr
 265 270 275

aaa gct ctg ggg tagaggctgg cgctgggact tgc 966
 Lys Ala Gly
 280

<210> 260

<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

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 20 25 30

Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro
 35 40 45

Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp
 50 55 60

Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser
 65 70 75 80

Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr
 85 90 95

Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val
 100 105 110

Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile
 115 120 125

Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala
 130 135 140

Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met
 145 150 155 160

Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe
 165 170 175

Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser

180	185	190
Phe Lys Gly Asp Lys Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu		
195	200	205
Pro Gly Thr Thr Gln Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly		
210	215	220
Trp Arg Cys Lys Glu Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala		
225	230	235
Asp Ser Val Trp Leu Val Ser Ser Val Arg Gly Pro Val Arg Val Thr		
245	250	255
Arg Leu Asp Gly His Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile		
260	265	270
Lys Ala Leu Ile Thr Lys Ala Leu Gly		
275	280	

<210> 261

<211> 1224

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1201)

<223> RXN01690

<400> 261

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Met Thr Ser Leu Glu	
1	5

ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag	163
Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys	
10	15
20	

gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg	211
Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met	
25	30
35	

gtg acc att gac tgg aac gag tgg gaa ggc tgg cac aac gcc caa tta	259
Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu	
40	45
50	

gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac	307
Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His	
55	60
65	

tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tgg gac	355
Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp	
70	75
80	85

gaa acc atc aag act ttc cct cct gat gaa aac gcc gag cgt atg cag	403
Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln	
90	95
100	

cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt	451
Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe	
105 110 115	
att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct	499
Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro	
120 125 130	
gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc	547
Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser	
135 140 145	
acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg	595
Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu	
150 155 160 165	
gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct	643
Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro	
170 175 180	
gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga	691
Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly	
185 190 195	
act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc	739
Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala	
200 205 210	
cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat	787
Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp	
215 220 225	
gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg	835
Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly	
230 235 240 245	
ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt	883
Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu	
250 255 260	
tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta	931
Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val	
265 270 275	
gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc	979
Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr	
280 285 290	
gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct	1027
Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala	
295 300 305	
tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct	1075
Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala	
310 315 320 325	
cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg	1123

His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac
 1171

Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga
 1221

Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 360 365

ccc
 1224

<210> 262

<211> 367

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser
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Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 195 200 205

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
 210 215 220

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly
 225 230 235 240

Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu
 245 250 255

Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
 260 265 270

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
 275 280 285

Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
 290 295 300

Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
 305 310 315 320

Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
 325 330 335

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
 340 345 350

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 355 360 365

<210> 263

<211> 1076

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1053)

<223> FRXA01690

<400> 263

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Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe	
1 5 10 15	
ttc acc gac cac atg gtg acc att gac tgg aac gag tcg gaa ggc tgg	96
Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp	
20 25 30	
cac aac gcc caa tta gtg cca tac gcg ccg att cct atg gat cct gcc	144
His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala	
35 40 45	
acc acc gta ttc cac tac gga cag gca att ttt gag gga att aag gcc	192
Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala	
50 55 60	
tac cgc cat tcg gac gaa acc atc aag act ttc cgt cct gat gaa aac	240
Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn	

65	70						75						80				
gcc Ala	gag Glu	cgt Arg	atg Met	cag Gln	cgt Arg	tca Ser	gca Ala	gct Ala	cga Arg	atg Met	gca Ala	atg Met	cca Pro	cag Gln	ttg Leu	288	
				85						90							
cca Pro	acc Thr	gag Glu	gac Asp	ttt Phe	att Ile	aaa Lys	gca Ala	ctt Leu	gaa Glu	ctg Leu	ctg Leu	gta Val	gac Asp	gcg Ala	gat Asp	336	
				100						105							
cag Gln	gat Asp	tgg Trp	gtt Val	cct Pro	gag Glu	tac Tyr	ggc Gly	gga Gly	gaa Glu	gct Ala	tcc Ser	ctc Leu	tac Tyr	ctg Leu	cgc Arg	384	
				115						120							
cca Pro	ttc Phe	atg Met	atc Ile	tcc Ser	acc Thr	gaa Glu	att Ile	ggc Gly	ttg Leu	ggg Gly	gtc Val	agc Ser	cca Pro	gct Ala	gat Asp	432	
				130						135							
gcc Ala	tac Tyr	aag Lys	ttc Phe	ctg Leu	gtc Val	atc Ile	gca Ala	tcc Ser	cca Pro	gtc Val	ggc Gly	gct Ala	tac Tyr	ttc Phe	acc Thr	480	
				145						150						155	
ggg Gly	gga Gly	atc Ile	aag Lys	cct Pro	gtt Val	tcc Ser	gtc Val	tgg Trp	ctg Leu	agc Ser	gaa Glu	gat Asp	tac Tyr	gtc Val	cgc Arg	528	
				165						170						175	
gct Ala	gca Ala	ccc Pro	ggc Gly	gga Gly	act Thr	ggg Gly	gac Asp	gcc Ala	aaa Lys	ttt Phe	gct Ala	ggc Gly	aac Asn	tac Tyr	cgc Ala	576	
				180						185						190	
gct Ala	tct Ser	ttg Leu	ctt Leu	gcc Ala	cag Gln	tcc Ser	cag Gln	gct Ala	gcg Ala	gaa Glu	aag Lys	ggc Gly	tgt Cys	gac Asp	cag Gln	624	
				195						200						205	
gtc Val	gta Val	tgg Trp	ttg Leu	gat Asp	gcc Ala	atc Ile	gag Glu	cac His	aag Lys	tac Tyr	atc Ile	gaa Glu	gaa Glu	atg Met	ggg Gly	672	
				210						215						220	
ggc Gly	atg Met	aac Asn	ctt Leu	ggg Gly	ttc Phe	atc Ile	tac Tyr	cgc Arg	aac Asn	ggc Gly	gac Asp	caa Gln	gtc Val	aag Lys	cta Leu	720	
				225						230						235	
gtc Val	acc Thr	cct Pro	gaa Glu	ctt Leu	tcc Ser	ggc Gly	tca Ser	cta Leu	ctt Leu	cca Pro	ggc Gly	atc Ile	acc Thr	cgc Arg	aag Lys	768	
				245						250						255	
tca Ser	ctt Leu	cta Leu	caa Gln	gta Val	gca Ala	cgc Arg	gac Asp	ttg Leu	gga Gly	tac Tyr	gaa Glu	gta Val	gaa Glu	gag Glu	cga Arg	816	
				260						265						270	
aag Lys	atc Ile	acc Thr	acc Thr	acc Thr	gag Glu	tgg Trp	gaa Glu	gaa Glu	gac Asp	gca Ala	aag Lys	tct Ser	ggc Gly	gcc Ala	atg Met	864	
				275						280						285	
acc Thr	gag Glu	gca Ala	ttt Phe	gct Ala	tgc Cys	ggg Gly	act Thr	gca Ala	gct Ala	gtt Val	atc Ile	acc Thr	cct Pro	gtt Val	ggc Gly	912	
				290						295						300	
acc Thr	gtg Val	aaa Lys	tca Ser	gct Ala	cac His	ggc Gly	acc Thr	ttc Phe	gaa Glu	gtg Val	aac Asn	aac Asn	aat Asn	gaa Glu	gtc Val	960	
				305						310						315	

gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa
1008

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
325 330 335

gga aac gtt gaa gac caa aac gga tgg ctt tac cca ctg gtt ggc
1053

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
340 345 350

taaatcaacc gggtttaaga ccc
1076

<210> 264

<211> 351

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
1 5 10 15

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
20 25 30

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
35 40 45

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
50 55 60

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
65 70 75 80

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
85 90 95

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
100 105 110

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
115 120 125

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
130 135 140

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
145 150 155 160

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
165 170 175

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
180 185 190

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Val Gly Cys Asp Gln
195 200 205

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly

<400>	265																
gaggtgacat ttatgcctct taatagctat actgtcccat gaaacgatat tttaatctca																	60
tatagtgaga tttacagatt tttaaaggac ggtgagttcc																	
											atg	acc	agc	ccc	gtg		115
											Met	Thr	Ser	Pro	Val		
											1					5	
gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg																	163
Glu	Asn	Ser	Thr	Ser	Thr	Glu	Lys	Leu	Thr	Leu	Ala	Glu	Lys	Val	Trp		
				10					15					20			
cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc																	211
Arg	Asp	His	Val	Val	Ser	Lys	Gly	Glu	Asn	Gly	Glu	Pro	Asp	Leu	Leu		
			25					30					35				
tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt																	259
Tyr	Ile	Asp	Leu	Gln	Leu	Leu	His	Glu	Val	Thr	Ser	Pro	Gln	Ala	Phe		
		40					45					50					
gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac																	307
Asp	Gly	Leu	Arg	Met	Thr	Gly	Arg	Lys	Leu	Arg	His	Pro	Glu	Leu	His		
	55					60					65						
ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc																	355

388

cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca gaa gac
1075

Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro Glu Asp
310 315 320 325

ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg cag tac
1123

Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu Gln Tyr
330 335 340

atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc
1171

Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr
345 350 355

gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc
1219

Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile
360 365 370

gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg
1267

Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met
375 380 385

atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc
1315

Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu
390 395 400 405

gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca
1363

Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala
410 415 420

ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc
1411

Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly
425 430 435

gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga
1459

Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly
440 445 450

cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc
1507

Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Ala Thr
455 460 465

gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga
1555

Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg
470 475 480 485

aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc
1603

Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys
490 495 500

agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca
1651

Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser
505 510 515

agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca act ggc
1699

Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly
520 525 530

gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg
1747

Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr
535 540 545

gct ccg ttc tcg tagcaggccc tgactttggc acc
1782

Ala Pro Phe Ser
550

<210> 266

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Met Thr Ser Pro Val Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu
1 5 10 15

Ala Glu Lys Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly
20 25 30

Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr
35 40 45

Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg
50 55 60

His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu
65 70 75 80

Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg
85 90 95

Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg
100 105 110

Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly
115 120 125

Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp
130 135 140

Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile
145 150 155 160

Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu
165 170 175

Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro

180	185	190
Gly Val Ser Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly 195 200 205		
Thr Gly Gly Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile 210 215 220		
Arg Lys Met Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile 225 230 235 240		
Glu Ala Gly Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe 245 250 255		
Asp Tyr Val Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp 260 265 270		
Glu Ala Val Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr 275 280 285		
Phe Asp Lys Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile 290 295 300		
Thr Trp Gly Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val 305 310 315 320		
Pro Ser Pro Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu 325 330 335		
Lys Ala Leu Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp 340 345 350		
Ile Lys Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile 355 360 365		
Glu Asp Leu Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala 370 375 380		
Asp Gly Met Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln 385 390 395 400		
Glu Ala Glu Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala 405 410 415		
Glu Trp Arg Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp 420 425 430		
Gln Leu Lys Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe 435 440 445		
Glu Gly Arg Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala 450 455 460		
Val Ala Ala Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr 465 470 475 480		
Leu Arg Lys Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala 485 490 495		
Leu Ala Phe His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser 500 505 510		

Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp
515 520 525

Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro
530 535 540

Thr Pro Thr Arg Thr Ala Pro Phe Ser
545 550

<210> 267

<211> 1625

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1602)

<223> FRXA01026

<400> 267

gtg tgg cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac 48
Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp
1 5 10 15

ctc ctc tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag 96
Leu Leu Tyr Ile Asp Leu Gln Leu His Glu Val Thr Ser Pro Gln
20 25 30

gca ttt gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa 144
Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu
35 40 45

ctg cac ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag 192
Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys
50 55 60

act ggc tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta 240
Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val
65 70 75 80

~~tct act ctg cgc gac aac tct gaa gaa ttc ggc gtg cgc ctg cac cca 288~~
Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro
85 90 95

atg ggt gat gtc cga cag ggc atc gtg cac acc gtc ggc cca cag ctc 336
Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu
100 105 110

ggc gca acc cag cca ggc atg acc att gtg tgc ggt gac tcc cac acc 384
Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr
115 120 125

tcc acc cac ggt gct ttt ggc tcc atg gca ttc ggc atc ggt acc tca 432
Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser
130 135 140

gag gtt gag cac gtc atg gct act caa acc ctg cca ctg aag cct ttc 480
Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe
145 150 155 160

aag acc atg gcc att gaa gtt act ggt gaa ctg cag cca ggt gtt tcc 528
Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser
165 170 175

tcc aag gac ctg att ctg gcg att atc gcc aag atc ggc acc ggc ggc 576
Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly
180 185 190

gga cag ggc tac gtt ctg gaa tac cgc ggc gaa gca atc cgt aag atg 624
Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met
195 200 205

tcc atg gat gca cgc atg acc atg tgc aac atg tcc atc gaa gct ggc 672
Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly
210 215 220

gca cgt gcc ggc atg atc gcc cca gac caa acc acc ttc gac tac gtt 720
Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val
225 230 235 240

gaa ggc cgc gaa atg gca cca aag ggc gcc gac tgg gac gaa gca gtt 768
Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val
245 250 255

gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag 816
Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys
260 265 270

gtc gta gaa atc gat ggc tcg gca ctg acc cca ttc atc acc tgg ggc 864
Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly
275 280 285

acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca 912
Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro
290 295 300

gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg 960
Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu
305 310 315 320

cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc
1008
Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile
325 330 335

gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg
1056
Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu
340 345 350

cag atc gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg
1104
Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
355 360 365

cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa
1152
Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
370 375 380

gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt
1200

Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
385 390 395 400

acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag
1248

Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
405 410 415

cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc
1296

Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
420 425 430

caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc
1344

Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
435 440 445

gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag
1392

Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
450 455 460

gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc
1440

Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
465 470 475 480

cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct
1488

His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
485 490 495

acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca
1536

Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
500 505 510

act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca
1584

Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
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1625

Arg Thr Ala Pro Phe Ser
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<210> 268

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

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Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln

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Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu 35 40 45		
Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys 50 55 60		
Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val 65 70 75 80		
Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro 85 90 95		
Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu 100 105 110		
Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr 115 120 125		
Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser 130 135 140		
Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe 145 150 155 160		
Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser 165 170 175		
Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly 180 185 190		
Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met 195 200 205		
Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly 210 215 220		
Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val 225 230 235 240		
Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val 245 250 255		
Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys 260 265 270		
Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly 275 280 285		
Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro 290 295 300		
Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu 305 310 315 320		
Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile 325 330 335		
Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu 340 345 350		

Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
 355 360 365

Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
 370 375 380

Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400

Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415

Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430

Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445

Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460

Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480

His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495

Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
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Arg Thr Ala Pro Phe Ser
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<210> 269
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN01127

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 Met Lys Leu Ala Val
 1 5
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
 10 15 20
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu

25	30	35	
ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat			259
Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp			
40	45	50	
ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt			307
Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly			
55	60	65	
gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg			355
Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu			
70	75	80	85
aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag			403
Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys			
90	95	100	
ctg tac gac ggc gtg gag tcc cca ctg cgt aac cca ggc aag att gat			451
Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn Pro Gly Lys Ile Asp			
105	110	115	
ttc gtt gtg gtc cgc gaa ggt acc gaa ggc gcc tac act ggc aac ggt			499
Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala Tyr Thr Gly Asn Gly			
120	125	130	
gga gca atc cgc gtg gga acc cct cac gag att gcc aat gaa acc tcc			547
Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile Ala Asn Glu Thr Ser			
135	140	145	
gtg aac act cgc tac ggc gct gag cgc gtt att cgc tac gca ttc gag			595
Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile Arg Tyr Ala Phe Glu			
150	155	160	165
ctg gca cag agc cgc cgc aag aag ctc acc ctc gtg cac aag acc aac			643
Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu Val His Lys Thr Asn			
170	175	180	
gtc ctg gtt cac ggt ggt ggc ctg tgg cag cgc acc gta gat gag gtt			691
Val Leu Val His Gly Gly Gly Leu Trp Gln Arg Thr Val Asp Glu Val			
185	190	195	
gca aag gaa tac cca gag gta gcc gtc gat tac aac cac atc gat gca			739
Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr Asn His Ile Asp Ala			
200	205	210	
gca acc atc tat ctg gtc act gat cct tcc cgc ttc gat gtg att gtt			787
Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg Phe Asp Val Ile Val			
215	220	225	
acc gat aac ctc ttc ggc gac atc ctc acc gat gag gca ggc gca gtc			835
Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp Glu Ala Gly Ala Val			
230	235	240	245
tct ggc gga att ggc ctc gca gca tcc ggc aac atc gat gcc acg ggc			883
Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn Ile Asp Ala Thr Gly			
250	255	260	
acc aac cct tcc atg ttc gag cca gtc cac ggc tct gca cca gat atc			931
Thr Asn Pro Ser Met Phe Glu Pro Val His Gly Ser Ala Pro Asp Ile			
265	270	275	

gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala
 280 285 290

atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa
 1027
 Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu
 295 300 305

aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att
 1075
 Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile
 310 315 320 325

tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc
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 Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
 330 335 340

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 1143

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 270
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Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
 35 40 45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
 50 55 60

~~Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu~~
 65 70 75 80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
 85 90 95

Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn
 100 105 110

Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala
 115 120 125

Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile
 130 135 140

Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile
 145 150 155 160

Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu

165 170 175
 Val His Lys Thr Asn Val Leu Val His Gly Gly Gly Leu Trp Gln Arg
 180 185 190
 Thr Val Asp Glu Val Ala Lys Glu Tyr Pro Glu Val Ala Val Asp Tyr
 195 200 205
 Asn His Ile Asp Ala Ala Thr Ile Tyr Leu Val Thr Asp Pro Ser Arg
 210 215 220
 Phe Asp Val Ile Val Thr Asp Asn Leu Phe Gly Asp Ile Leu Thr Asp
 225 230 235 240
 Glu Ala Gly Ala Val Ser Gly Gly Ile Gly Leu Ala Ala Ser Gly Asn
 245 250 255
 Ile Asp Ala Thr Gly Thr Asn Pro Ser Met Phe Glu Pro Val His Gly
 260 265 270
 Ser Ala Pro Asp Ile Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala
 275 280 285
 Ile Leu Ser Ala Ala Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn
 290 295 300
 Ala Val Arg Ile Glu Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp
 305 310 315 320
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 325 330 335
 Ala Leu Gln Ser
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 <223> FRXA01132

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 Met Lys Leu Ala Val
 1 5
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
 10 15 20
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu
 25 30 35

aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403
Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys
90 95 100

<213> Corynebacterium glutamicum

Leu Arg Pro Ser Lys
100

<213> Corynebacterium glutamicum

<223> RXN00536

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tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115
Met Ser Pro Asn Asp
1 5

gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc 163
 Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg
 10 15 20

aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca 211
 Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro
 25 30 35

gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg 259
 Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu
 40 45 50

ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg 307
 Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp
 55 60 65

tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg 355
 Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met
 70 75 80 85

tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc 403
 Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly
 90 95 100

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 Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe
 105 110 115

gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc 499
 Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val
 120 125 130

acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act 547
 Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr
 135 140 145

ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac 595
 Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn
 150 155 160 165

tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg 643
 Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val
 170 175 180

cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc 691
 Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile
 185 190 195

gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag 739
 Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu
 200 205 210

tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca 787
 Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala
 215 220 225

gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac 835
 Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn
 230 235 240 245

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc 883
 Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser
 250 255 260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg 931
 Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc
 1027
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac
 1075
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc
 1123
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag
 1171
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc
 1219
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt
 1267
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
 375 380 385

~~cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg aga gaa~~
 1315
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
 390 395 400 405

acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg
 1363
 Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg
 410 415 420

tcg cga cta cga ggc tgt tat ccg cgt gaa ctg cca gtc cgg caa ggg
 1411
 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly
 425 430 435

cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg
 1459
 Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser
 440 445 450

ctc cat gca ggt tgagttctcc accggtgtcc aga

1494

Leu His Ala Gly

455

<210> 274

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val

35 40 45

Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr

50 55 60

Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala

65 70 75 80

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu

85 90 95

Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala

100 105 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met

115 120 125

Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His

130 135 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile

145 150 155 160

Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe

165 170 175

Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu

180 185 190

Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp

195 200 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys

210 215 220

Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn

225 230 235 240

Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn

245 250 255

Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg
260 265 270

Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly
275 280 285

Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu
290 295 300

Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val
305 310 315 320

Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp
325 330 335

Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln
340 345 350

Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr
355 360 365

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
385 390 395 400

Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg
405 410 415

Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu
420 425 430

Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg
435 440 445

Ser Ala Asp Pro Ser Leu His Ala Gly
450 455

<210> 275

<211> 1333

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1333)

<223> FRXA00536

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Met Ser Pro Asn Asp
1 5

gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc 163
Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg
10 15 20

aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca 211
 Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro
 25 30 35

gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg 259
 Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu
 40 45 50

ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg 307
 Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp
 55 60 65

tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg 355
 Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met
 70 75 80 85

tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc 403
 Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly
 90 95 100

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 Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe
 105 110 115

gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc 499
 Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val
 120 125 130

acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act 547
 Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr
 135 140 145

ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac 595
 Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn
 150 155 160 165

tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg 643
 Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val
 170 175 180

cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc 691
 Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile
 185 190 195

gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag 739
 Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu
 200 205 210

tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca 787
 Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala
 215 220 225

gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac 835
 Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn
 230 235 240 245

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc 883
 Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser
 250 255 260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg 931

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Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
      265                      270                      275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag      979
Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
      280                      285                      290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc
1027
Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
      295                      300                      305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac
1075
Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
      310                      315                      320                      325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc
1123
Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
      330                      335                      340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag
1171
Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
      345                      350                      355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc
1219
Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
      360                      365                      370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt
1267
His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
      375                      380                      385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac
1315
Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
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acc gaa tgg gag gtt cct
1333
Thr Glu Trp Glu Val Pro
      410

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<210> 276

<211> 411

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

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Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr
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Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg
      20                      25                      30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val

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35	40	45
Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr 50 55 60		
Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala 65 70 75 80		
Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu 85 90 95		
Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala 100 105 110		
Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met 115 120 125		
Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His 130 135 140		
Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile 145 150 155 160		
Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe 165 170 175		
Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu 180 185 190		
Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp 195 200 205		
Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys 210 215 220		
Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn 225 230 235 240		
Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn 245 250 255		
Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg 260 265 270		
Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly 275 280 285		
Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu 290 295 300		
Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val 305 310 315 320		
Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp 325 330 335		
Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln 340 345 350		
Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr 355 360 365		

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
385 390 395 400

Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro
405 410

<210> 277

<211> 714

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

<400> 277

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ctgtcctcac ctgcagatat ctaaggaagg ctagaaaaca atg gaa aaa ttt acc 115
Met Glu Lys Phe Thr
1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163
Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr
10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211
Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly
25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259
Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe
40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307
Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly
55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355
Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu
70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403
Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile
90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451
Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu
105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499
Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly
120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp
 135 140 145
 gta gtg atc agc ttc gaa gtt gac ccc tac atc cgc tgg cgt ttg atg 595
 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met
 150 155 160 165
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile
 170 175 180
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala
 185 190 195
 taagtttcag tctgatagcg aaa 714

<210> 278

<211> 197

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 278

Met Glu Lys Phe Thr Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg
 1 5 10 15

Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg
 20 25 30

Val Thr Arg Thr Gly Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln
 35 40 45

Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser
 50 55 60

Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His
 65 70 75 80

Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser
 85 90 95

Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu
 100 105 110

Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met
 115 120 125

Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile
 130 135 140

Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile
 145 150 155 160

Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg
 165 170 175

Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys
 180 185 190

Pro Arg Thr Asn Ala

195

<210> 279
 <211> 936
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(913)
 <223> RXN01929

<400> 279
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ggaattttatt tattctgagc tggatcatcac atctatactc atg ccc atg tca ggc 115
 Met Pro Met Ser Gly
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
 135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
 Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
 150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643

Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 280
 <211> 271
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280
 Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
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Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
 20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

130	135	140
His Ile Gly Tyr Thr	Pro Gln Ser Glu His	Ser Leu Gly Gly His Val
145	150	155 160
Val Gln Gly Arg Gly	Ala Ser Ser Gly Lys	Leu Ile Ala Asp Ala Arg
165	170	175
Ala Leu Glu Gln Ala	Gly Ala Phe Ala	Val Val Leu Glu Met Val Pro
180	185	190
Ala Glu Ala Ala Arg	Glu Val Thr Glu Asp	Leu Ser Ile Thr Thr Ile
195	200	205
Gly Ile Gly Ala Gly	Asn Gly Thr Asp Gly	Gln Val Leu Val Trp Gln
210	215	220
Asp Ala Phe Gly Leu	Asn Arg Gly Lys Lys	Pro Arg Phe Val Arg Glu
225	230	235 240
Tyr Ala Thr Leu Gly	Asp Ser Leu His Asp	Ala Ala Gln Ala Tyr Ile
245	250	255
Ala Asp Ile His Ala	Gly Thr Phe Pro Gly	Glu Ala Glu Ser Phe
260	265	270

<210> 281

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> FRXA01929

<400> 281

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tatttattct	gagctgggtca	tcacatctat	actcatgccc	atg tca ggc att gat	115
				Met Ser Gly Ile Asp	
				1 5	

gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly	
10 15 20	

cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile	
25 30 35	

ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala	
40 45 50	

aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu	
55 60 65	

atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355
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Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu
 70 75 80 85

gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag 403
 Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln
 90 95 100

gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg 451
 Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala
 105 110 115

gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att 499
 Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile
 120 125 130

gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag 547
 Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln
 135 140 145

tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt 595
 Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser
 150 155 160 165

tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg 643
 Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala
 170 175 180

ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt 691
 Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val
 185 190 195

acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc 739
 Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly
 200 205 210

aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc 787
 Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg
 215 220 225

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
 Phe Pro Gly Glu Ala Glu Ser Phe
 265

<210> 282

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu
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Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
 225 230 235 240
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
 245 250 255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265

<210> 283

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXN01420

<400> 283

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gcggaatgcg	ctgctcatcc	acacgtggaa	tcccgattgg	gtg	acg	ctg	ggt	gga												115
				Val	Thr	Leu	Gly	Gly												
				1				5												
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	gcg	gaa	atg	ctg	ttc	tac	ctg					163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	Ala	Glu	Met	Leu	Phe	Tyr	Leu					
				10				15						20						
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	cgc	aaa	gtg	aag	ggc	gtg	ggc					211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	Arg	Lys	Val	Lys	Gly	Val	Gly					
			25				30						35							
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	gcc	gtg	agc	ctg	gcg	ctg	att					259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	Ala	Val	Ser	Leu	Ala	Leu	Ile					
			40				45					50								
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	cca	aag	ggg	att	gag	aac	ttc					307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	Pro	Lys	Gly	Ile	Glu	Asn	Phe					
	55					60					65									
ttt	gtt	cct	cgc	ctg	tgg	gac	acc	aat	gtg	tca	ccg	gtc	gcg	gaa	gtt					355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	Val	Ser	Pro	Val	Ala	Glu	Val					
	70				75				80						85					
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	gaa	gaa	att	ccc	gtg	ctg	gaa					403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	Glu	Glu	Ile	Pro	Val	Leu	Glu					
				90				95						100						
tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	ctg	acc	aga	ctc	atc	gag	ttc					451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	Leu	Thr	Arg	Leu	Ile	Glu	Phe					
			105				110						115							
tac	ctc	ggt	gtg	ttt	ggc	gcg	aag	ctg	gtt	gct	gaa	ggc	atg	ttt	aaa					499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	Val	Ala	Glu	Gly	Met	Phe	Lys					
			120				125					130								
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	gca	ctg	gct	gtt	tct	ttt	gtt					547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	Ala	Leu	Ala	Val	Ser	Phe	Val					
			135			140					145									
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	aag	atg	tct	gtc	atc	atg	tcc					595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	Lys	Met	Ser	Val	Ile	Met	Ser					
	150				155					160					165					
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	ctt	gcg	gtg	aga	gac	att	gaa					643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala													

ttc tat gca gtg gtg tgt ttc atc gtg tcg gtc att ctc gcg tgg gtg 835
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val
 230 235 240 245

ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys
 250 255 260

aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu
 265 270 275

aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr
 280 285 290

cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct
 1027
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala
 295 300 305

acc gga atc aaa tct tagggaagga aaacatatgg cta
 1065
 Thr Gly Ile Lys Ser
 310

<210> 284

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu
 1 5 10 15

Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys
 20 25 30

Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val
 35 40 45

Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys
 50 55 60

Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser
 65 70 75 80

Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu
 85 90 95

Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr
 100 105 110

Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala
 115 120 125

Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu
 130 135 140

Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met

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<210> 285
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1114)
<223> RXS01145
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<400> 285
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cttttcacca aaattttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
                                         Met Ala Ile Glu Leu
                                         1                               5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
                        10                               15                   20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
                        25                               30                   35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
                        40                               45                   50

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tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
ggt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
330 335

ccctttgacg gct
1137

<210> 286

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 286

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
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Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335
 Thr Ala

<210> 287

<211> 556

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> FRXA01145

<400> 287

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cttttcacca aaattttttac gaaaggcgag atttttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
 135 140 145

tgc ctc atc 556
 Cys Leu Ile
 150

<210> 288

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
 1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 289

<211> 1350

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02375

<400> 289

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aagcggttcga ttacgggata atctcccaac gccaacccaa atg gcg ccg gtg aca 115
Met Ala Pro Val Thr
1 5

ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser
10 15 20

ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His
25 30 35

gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val
40 45 50

aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val
55 60 65

gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met
70 75 80 85

gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403
~~Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala~~
90 95 100

gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val
105 110 115

aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499
Lys Gln Ala Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp
120 125 130

gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu
135 140 145

acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg
150 155 160 165

acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa 643
 Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu
 170 175 180

aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga 691
 Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg
 185 190 195

ctt gct gca att gtg gcg cac ctg gtg tcg gct gat gct ttg gtg ctg 739
 Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu
 200 205 210

ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc 787
 Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr
 215 220 225

gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc 835
 Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val
 230 235 240 245

att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag 883
 Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys
 250 255 260

gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg 931
 Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu
 265 270 275

acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc 979
 Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly
 280 285 290

act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg
 1027
 Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp
 295 300 305

gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc
 1075
 Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly
 310 315 320 325

gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc
 1123
 Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly
 330 335 340

att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc
 1171
 Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile
 345 350 355

ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat
 1219
 Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp
 360 365 370

tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca
 1267
 Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro
 375 380 385

gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac
1315

Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr
390 395 400 405

gcc agc cgc gcg taaagcgcgg gcctgctggt gcc
1350

Ala Ser Arg Ala

<210> 290

<211> 409

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 290

Met Ala Pro Val Thr Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala
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Ser Ile Gly Ala Ser Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser
20 25 30

Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala
35 40 45

Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu
50 55 60

Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala
65 70 75 80

Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser
85 90 95

Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro
100 105 110

Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Val Gly Gln Val His
115 120 125

~~Leu Met His Gln Thr Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile~~
~~130 135 140~~

Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala
145 150 155 160

Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val
165 170 175

Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe
180 185 190

Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala
195 200 205

Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn
210 215 220

Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn

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<400> 291
gagcagatgg ccaccgaggt cgatgtggtg gctggctact aggcctttta tgggtgtgac 60
cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
Met Ser Ser Thr Thr
1 5
cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
10 15 20
aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
Lys Ala Thr Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
25 30 35

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acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt	259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val	
40 45 50	
gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg	307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala	
55 60 65	
ggg cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt	355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu	
70 75 80 85	
gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct	403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala	
90 95 100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa	451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu	
105 110 115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc	499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly	
120 125 130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg	547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu	
135 140 145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct	595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala	
150 155 160 165	
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag	643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu	
170 175 180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc	691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr	
185 190 195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg	739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val	
200 205 210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt	787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly	
215 220 225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac	835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr	
230 235 240 245	
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac	883
Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn	
250 255 260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt	931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu	
265 270 275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg	979

Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala
 280 285 290

ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa
 1027

Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu
 295 300 305

gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat
 1075

Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp
 310 315 320 325

tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg
 1123

Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val
 330 335 340

gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa
 1171

Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu
 345 350 355

gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc
 1219

Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg
 360 365 370

gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat
 1267

Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp
 375 380 385

ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa
 1315

Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys
 390 395 400 405

ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag
 1363

Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys
 410 415 420

tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca
 1416

Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro
 425 430

agc
 1419

<210> 292

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

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 20 25 30
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val
 130 135 140
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg
 195 200 205
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn
 210 215 220
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly
 225 230 235 240
~~Asp Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile~~
~~245 250 255~~
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala
 260 265 270
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu
 275 280 285
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg
 290 295 300
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr
 305 310 315 320
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala
 325 330 335
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser

340	345	350
Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln		
355	360	365
Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser		
370	375	380
Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly		
385	390	395
Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu		
405	410	415
Leu Thr Ser Thr Lys Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro		
420	425	430

<210> 293
 <211> 724
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(709)
 <223> FRXA02378

<400> 293
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cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
 Met Ser Ser Thr Thr
 1 5

cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
 10 15 20

aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val
 40 45 50

gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala
 55 60 65

ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu
 70 75 80 85

gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala
 90 95 100

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451
 Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu
 105 110 115
 aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499
 Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly
 120 125 130
 atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547
 Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu
 135 140 145
 gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595
 Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala
 150 155 160 165
 gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643
 Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu
 170 175 180
 cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691
 Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro
 185 190 195
 gcg gat ccg tcc aag att tgatcacccgg acgcg 724
 Ala Asp Pro Ser Lys Ile
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<210> 294

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
 1 5 10 15

Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp
 20 25 30

~~Ile Ala Val Leu Gly Thr Gly Pro Lys Ser Ala Ile Leu Arg Ala Ala~~
 35 40 45

Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60

Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80

Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95

Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110

Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125

Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val

130 135 140
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile
 195 200

<210> 295

<211> 623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(600)

<223> FRXA02382

<400> 295

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 Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala
 1 5 10 15

gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc 96
 Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
 20 25 30

cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc 144
 Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
 35 40 45

gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa 192
 Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
 50 55 60

gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt 240
 Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
 65 70 75 80

gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac 288
 Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
 85 90 95

ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct 336
 Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
 100 105 110

ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc 384
 Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
 115 120 125

acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca 432
 Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
 130 135 140

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
 180 185 190

cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca agc 623
 Gln Gly Thr Gly Gln Ile Arg Pro
 195 200

<210> 296

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala
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Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
 20 25 30

Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
 35 40 45

Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
 50 55 60

Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
 65 70 75 80

Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
 85 90 95

~~Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala~~
 100 105 110

Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
 115 120 125

Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
 130 135 140

Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160

Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175

Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
 180 185 190

Gln Gly Thr Gly Gln Ile Arg Pro

195

200

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<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(910)
<223> RXA02499
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ctgctgcaaaa acaggggttg ttagtggcag tgtgggaacc atg aca aca att gct Met Thr Thr Ile Ala 1 5	115
. gta atc ggc ggc gga caa atc ggc gag gct tta gtc tca ggt ttg atc Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu Val Ser Gly Leu Ile 10 15 20	163
gcg gcc aac atg aat cca caa aat att cgc gtc acc aac cgt tcg gaa Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val Thr Asn Arg Ser Glu 25 30 35	211
gag cgc ggc caa gag ctg cgt gac cgc tac ggc atc ctc aac atg acg Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly Ile Leu Asn Met Thr 40 45 50	259
gat aat tcc caa gcc gca gac gaa gcc gac gtg gtg ttc ctg tgc gtg Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val Val Phe Leu Cys Val 55 60 65	307
aag ccg aaa ttt atc gtc gaa gtg ctc tcc gaa atc acc ggc act ttg Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu Ile Thr Gly Thr Leu 70 75 80 85	355
gat aac aac tcc gca caa agt gtt gtg gtc agc atg gcc gca ggc atc Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser Met Ala Ala Gly Ile 90 95 100	403
agc atc gct gcc atg gaa gaa agc gcc tct gcg ggg ctc ccc gtc gtg Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala Gly Leu Pro Val Val 105 110 115	451
cgc gtc atg ccg aac act cca atg ctc gtg ggc aag ggc atg tcg act Arg Val Met Pro Asn Thr Pro Met Leu Val Gly Lys Gly Met Ser Thr 120 125 130	499
gtc acc aaa ggc cgc tac gtt gac gcg gaa cag ttg gaa caa gtc aag Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln Leu Glu Gln Val Lys 135 140 145	547
gac ttg ttg agc acc gtt gga gac gtc ctc gaa gtc gcg gaa tca gac Asp Leu Leu Ser Thr Val Gly Asp Val Leu Val Ala Glu Ser Asp 150 155 160 165	595
atc gac gca gtc acc gcg atg tcc gga tcc tcc cct gca tac ctg ttc	643

Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe
 170 175 180

ctt gtg acc gaa gcg ctc att gag gca gga gtt aat cta ggc ctg ccc 691
 Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro
 185 190 195

cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca 739
 Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala
 200 205 210

acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc 787
 Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly
 215 220 225

gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa 835
 Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu
 230 235 240 245

gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc 883
 Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala
 250 255 260

gac cga tct gaa gaa ctc gga aag cgc tagaaaccgt tatttccccg 930
 Asp Arg Ser Glu Glu Leu Gly Lys Arg
 265 270

tta 933

<210> 298

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

Met Thr Thr Ile Ala Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu
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Val Ser Gly Leu Ile Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val
 20 25 30

Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Thr Gly
 35 40 45

Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val
 50 55 60

Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu
 65 70 75 80

Ile Thr Gly Thr Leu Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser
 85 90 95

Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala
 100 105 110

Gly Leu Pro Val Val Arg Val Met Pro Asn Thr Pro Met Leu Val Gly
 115 120 125

Lys Gly Met Ser Thr Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln

130					135					140					
Leu	Glu	Gln	Val	Lys	Asp	Leu	Leu	Ser	Thr	Val	Gly	Asp	Val	Leu	Glu
145					150					155					160
Val	Ala	Glu	Ser	Asp	Ile	Asp	Ala	Val	Thr	Ala	Met	Ser	Gly	Ser	Ser
				165					170					175	
Pro	Ala	Tyr	Leu	Phe	Leu	Val	Thr	Glu	Ala	Leu	Ile	Glu	Ala	Gly	Val
			180					185						190	
Asn	Leu	Gly	Leu	Pro	Arg	Ala	Thr	Ala	Lys	Lys	Leu	Ala	Val	Ala	Ser
		195					200					205			
Phe	Glu	Gly	Ala	Ala	Thr	Met	Met	Lys	Glu	Thr	Gly	Lys	Glu	Pro	Ser
	210					215					220				
Glu	Leu	Arg	Ala	Gly	Val	Ser	Ser	Pro	Ala	Gly	Thr	Thr	Val	Ala	Ala
225					230					235					240
Ile	Arg	Glu	Leu	Glu	Glu	Ser	Gly	Ile	Arg	Gly	Ala	Phe	Tyr	Arg	Ala
				245					250					255	
Ala	Gln	Ala	Cys	Ala	Asp	Arg	Ser	Glu	Glu	Leu	Gly	Lys	Arg		
			260					265					270		

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<210> 299
<211> 1296
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1273)
<223> RXS02157
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caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa	115
Met Ser Thr Leu Glu	
1 5	
act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag	163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu	
10 15 20	
ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc	211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val	
25 30 35	
tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc	259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala	
40 45 50	
cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt	307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly	
55 60 65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag	355

His	Val	Ser	Asn	Leu	Phe	Ala	Ser	Arg	Pro	Val	Val	Glu	Val	Ala	Glu	
70					75					80					85	
gag	ctc	atc	aag	cgt	ttt	tcg	ctt	gac	gac	gcc	acc	ctc	gcc	gcg	caa	403
Glu	Leu	Ile	Lys	Arg	Phe	Ser	Leu	Asp	Asp	Ala	Thr	Leu	Ala	Ala	Gln	
			90					95						100		
acc	cgg	gtt	ttc	ttc	tgc	aac	tcg	ggc	gcc	gaa	gca	aac	gag	gct	gct	451
Thr	Arg	Val	Phe	Phe	Cys	Asn	Ser	Gly	Ala	Glu	Ala	Asn	Glu	Ala	Ala	
			105					110					115			
ttc	aag	att	gca	cgc	ttg	act	ggg	cgt	tcc	cgg	att	ctg	gct	gca	gtt	499
Phe	Lys	Ile	Ala	Arg	Leu	Thr	Gly	Arg	Ser	Arg	Ile	Leu	Ala	Ala	Val	
		120					125					130				
cat	ggg	ttc	cac	ggc	cgc	acc	atg	ggg	tcc	ctc	gcg	ctg	act	ggc	cag	547
His	Gly	Phe	His	Gly	Arg	Thr	Met	Gly	Ser	Leu	Ala	Leu	Thr	Gly	Gln	
	135					140					145					
cca	gac	aag	cgt	gaa	gcg	ttc	ctg	cca	atg	cca	agc	ggg	gtg	gag	ttc	595
Pro	Asp	Lys	Arg	Glu	Ala	Phe	Leu	Pro	Met	Pro	Ser	Gly	Val	Glu	Phe	
150				155						160					165	
tac	cct	tac	ggc	gac	acc	gat	tac	ttg	cgc	aaa	atg	gta	gaa	acc	aac	643
Tyr	Pro	Tyr	Gly	Asp	Thr	Asp	Tyr	Leu	Arg	Lys	Met	Val	Glu	Thr	Asn	
			170					175						180		
cca	acg	gat	gtg	gct	gct	atc	ttc	ctc	gag	cca	atc	cag	ggg	gaa	acg	691
Pro	Thr	Asp	Val	Ala	Ala	Ile	Phe	Leu	Glu	Pro	Ile	Gln	Gly	Glu	Thr	
			185					190					195			
ggc	gtt	gtt	cca	gca	cct	gaa	gga	ttc	ctc	aag	gca	gtg	cgc	gag	ctg	739
Gly	Val	Val	Pro	Ala	Pro	Glu	Gly	Phe	Leu	Lys	Ala	Val	Arg	Glu	Leu	
		200					205					210				
tgc	gat	gag	tac	ggc	atc	ttg	atg	atc	acc	gat	gaa	gtc	cag	act	ggc	787
Cys	Asp	Glu	Tyr	Gly	Ile	Leu	Met	Ile	Thr	Asp	Glu	Val	Gln	Thr	Gly	
	215					220					225					
gtt	ggc	cgt	acc	ggc	gat	ttc	ttt	gca	cat	cag	cac	gat	ggc	gtt	gtt	835
Val	Gly	Arg	Thr	Gly	Asp	Phe	Phe	Ala	His	Gln	His	Asp	Gly	Val	Val	
230					235					240					245	
ccc	gat	gtg	gtg	acc	atg	gcc	aag	gga	ctt	ggc	ggc	ggg	ctt	ccc	atc	883
Pro	Asp	Val	Val	Thr	Met	Ala	Lys	Gly	Leu	Gly	Gly	Gly	Leu	Pro	Ile	
				250					255					260		
ggg	gct	tgt	ttg	gcc	act	ggc	cgt	gca	gct	gaa	ttg	atg	acc	cca	ggc	931
Gly	Ala	Cys	Leu	Ala	Thr	Gly	Arg	Ala	Ala	Glu	Leu	Met	Thr	Pro	Gly	
			265					270					275			
aag	cac	ggc	acc	act	ttc	ggg	ggc	aac	cca	gtt	gct	tgt	gca	gct	gcc	979
Lys	His	Gly	Thr	Thr	Phe	Gly	Gly	Asn	Pro	Val	Ala	Cys	Ala	Ala	Ala	
		280					285					290				
aag	gca	gtg	ctg	tct	gtt	gtc	gat	gac	gct	ttc	tgc	gca	gaa	gtt	gcc	
1027																
Lys	Ala	Val	Leu	Ser	Val	Val	Asp	Asp	Ala	Phe	Cys	Ala	Glu	Val	Ala	
	295					300					305					

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
1075

Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
1123

Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
1171

Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
1219

Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
1267

Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
375 380 385

atc gca taaaggactc aaacttatga ctt
1296

Ile Ala
390

<210> 300

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

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Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
35 40 45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
50 55 60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
65 70 75 80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
85 90 95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
100 105 110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
115 120 125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asp Ile Ile Arg Leu
 355 360 365
 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
 370 375 380
 Ala Ile Ala Glu Thr Ile Ala
 385 390

<210> 301
 <211> 1269
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1246)
 <223> RXS02262

<400> 301

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tcgataagca aaaaatcgct gatactcgaa aggcctcaaa atg acc gca acc tac 115
 Met Thr Ala Thr Tyr
 1 5

acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
 10 15 20

atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
 25 30 35

gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
 40 45 50

aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
 55 60 65

ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
 70 75 80 85

ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
 Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
 90 95 100

gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451
 Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His
 105 110 115

acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499
 Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met
 120 125 130

tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547
 Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val
 135 140 145

ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595
 Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val
 150 155 160 165

gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643
 Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu
 170 175 180

cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc 691
 Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly
 185 190 195

atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa 739
 Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu
 200 205 210

gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc 787

Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile
 215 220 225
 gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca 835
 Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro
 230 235 240 245
 tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca 883
 Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro
 250 255 260
 gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc 931
 Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu
 265 270 275
 gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc 979
 Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly
 280 285 290
 cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac
 1027
 Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp
 295 300 305
 ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc
 1075
 Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly
 310 315 320 325
 gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc
 1123
 Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile
 330 335 340
 atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca
 1171
 Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala
 345 350 355
 acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg
 1219
 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu
 360 365 370

aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg
 1266
 Asn Leu Trp Glu Ser Pro Ala Leu Ala
 375 380

aaa
 1269

<210> 302
 <211> 382
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 302
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 20 25 30
 Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr
 35 40 45
 Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
 50 55 60
 Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
 65 70 75 80
 Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
 85 90 95
 Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
 100 105 110
 Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
 115 120 125
 Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
 130 135 140
 Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
 145 150 155 160
 Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
 165 170 175
 Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
 180 185 190
 Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
 195 200 205
 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
 210 215 220
 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
 225 230 235 240
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
 245 250 255
 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
 260 265 270
 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335

Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
340 345 350

Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
355 360 365

Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
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<211> 1491

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<220>

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<222> (101)..(1468)

<223> RXS02970

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ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly

135	140	145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga			595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly			
150	155	160	165
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc			643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr			
170	175		180
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc			691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser			
185	190		195
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag			739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys			
200	205		210
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg			787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala			
215	220		225
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca			835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro			
230	235		245
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc			883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile			
250	255		260
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa			931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys			
265	270		275
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc			979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile			
280	285		290
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc			1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile			
295	300		305
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc			1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser			
310	315		325
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag			1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys			
330	335		340
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct			1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala			
345	350		355
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa			1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu			

360 365 370
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 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385
 gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405
 ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420
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 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435
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 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450
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 1491
 Ala Leu Phe
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<210> 304
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 <213> Corynebacterium glutamicum

<400> 304
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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe

115	120	125
Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala		
130	135	140
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr		
145	150	155
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg		
165	170	175
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro		
180	185	190
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys		
195	200	205
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala		
210	215	220
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly		
225	230	235
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys		
245	250	255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe		
260	265	270
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe		
275	280	285
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala		
290	295	300
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly		
305	310	315
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala		
325	330	335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile		
340	345	350
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu		
355	360	365
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile		
370	375	380
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala		
385	390	395
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser		
405	410	415
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu		
420	425	430
Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu		
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Leu Thr Phe Ala Gly Ala Leu Phe
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<213> Corynebacterium glutamicum

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<223> FRXA01009

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Leu Ala Leu Lys Gly 5
1
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala 20
10 15
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe 35
25 30
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala 50
40 45
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp 65
55 60
atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg 85
70 75 80
~~tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg aag aac atc aac 403~~
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn 100
90 95
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val 115
105 110
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly 130
120 125
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly 145
135 140
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly 165
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
 Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
 185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
 Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
 200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
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375          380          385
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390          395          400          405

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Phe Lys Glu Arg Gly
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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35      40      45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50      55      60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65      70      75      80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85      90      95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100     105     110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115     120     125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130     135     140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145     150     155     160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165     170     175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180     185     190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195     200     205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
210     215     220

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 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
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 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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<210> 307

<211> 3579

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(3556)

<223> RXN00023

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 Met Thr Ser Met Asn
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 10 15 20

cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat 211
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Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
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Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
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Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
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Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
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Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
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Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcc atc	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
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Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
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Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala	
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Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883
Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
250 255 260	
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Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg	
265 270 275	

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 280 285 290

ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg
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 295 300 305

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 1075
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc
 1123
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg
 1171
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu
 345 350 355

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 360 365 370

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 1267
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly
 375 380 385

gag ctg ctg ctt tac gta cca gcc gtg cgc cca caa gaa ttc gac gtg
 1315
 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val
 390 395 400 405

gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa
 1363
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 410 415 420

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 1411
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe
 425 430 435

aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg
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 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr
 440 445 450

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 1507
 Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser
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aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc
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Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro
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1603

Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala
490 495 500

gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg
1651

Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro
505 510 515

gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc
1699

Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg
520 525 530

gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag
1747

Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu
535 540 545

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1795

Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu
550 555 560 565

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1843

Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp
570 575 580

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1891

Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu
585 590 595

gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc
1939

Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg
600 605 610

gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct
1987

Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala
615 620 625

gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa
2035

Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys
630 635 640 645

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc
2083

Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu
650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct
2131

Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala

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665          670          675
aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc
2179
Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg
680          685          690

gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg
2227
Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp
695          700          705

cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc
2275
Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile
710          715          720          725

gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg
2323
Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val
730          735          740

aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc
2371
Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu
745          750          755

ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag
2419
Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln
760          765          770

ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc
2467
Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro
775          780          785

tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac
2515
Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His
790          795          800          805

cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc
2563
His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro
810          815          820

cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa
2611
Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu
825          830          835

ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca
2659
Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro
840          845          850

gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc
2707
Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe
855          860          865

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caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala
890 895 900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc
2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca
3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat
3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga
3139

Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg
1000 1005 1010

ctc gac gat tcc gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca
3187

Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala
1015 1020 1025

gcc cgt cgc gcc ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt
3235

Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val
1030 1035 1040 1045

tca gag caa gtc cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa
3283

Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu
1050 1055 1060

aca gtc gat gat tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac
3331

Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr
1065 1070 1075

gac gag aac tcc agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac
3379

Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp
1080 1085 1090

act gtc cgt gaa cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac
3427

Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp
1095 1100 1105

gat gca gta act gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa
3475

Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys
1110 1115 1120 1125

gaa caa gca att tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg
3523

Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala
1130 1135 1140

gcc ttc cac gag ttg gcg gag gaa ctt aaa cgt tgatcgtttt gcgcatgggt
3576

Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg
1145 1150

cgc
3579

<210> 308

<211> 1152

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

Met Thr Ser Met Asn Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln
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Ala Val Asp Lys Val Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser
20 25 30

Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
50 55 60

Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
100 105 110

Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
 195 200 205
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
 210 215 220
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
 225 230 235 240
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
 260 265 270
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala
 290 295 300
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr
 305 310 315 320
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
~~Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile~~
~~340 345 350~~
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro
 385 390 395 400
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu
 405 410 415
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala
 420 425 430
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile

435	440	445
Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His		
450	455	460
Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro		
465	470	475
Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln		
	485	490
Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu		
	500	505
Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu		
	515	520
Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala		
	530	535
Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val		
	545	550
Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala		
	565	570
Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg		
	580	585
Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu		
	595	600
Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro		
	610	615
Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala		
	625	630
Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala		
	645	650
Val Val Glu Ala Leu Trp Glu Ala Gly Val Pro Arg Glu Val Leu His		
	660	665
Cys Ile Tyr Pro Ala Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His		
	675	680
Glu His Val Asp Arg Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala		
	690	695
Met Phe Ser Ser Trp Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser		
	705	710
Gly Lys Asn Ala Ile Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala		
	725	730
Val Ala Asp Leu Val Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys		
	740	745
Ser Ala Ala Ser Leu Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu		
	755	760

Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp
 770 775 780
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro
 785 790 795 800
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser
 805 810 815
 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser
 820 825 830
 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr
 835 840 845
 Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn
 850 855 860
 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly
 865 870 875 880
 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val
 885 890 895
 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val
 900 905 910
 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly
 915 920 925
 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala
 930 935 940
 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser
 945 950 955 960
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn
 965 970 975
 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
 980 985 990
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005
 Glu Val Val Leu Arg Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala
 1010 1015 1020
 Arg Ala Leu Leu Ala Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu
 1025 1030 1035 1040
 Gln Thr Pro Gly Val Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala
 1045 1050 1055
 Gly Val Ser Ala Glu Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val
 1060 1065 1070
 Leu Arg Gly Glu Tyr Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu
 1075 1080 1085

Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu
1090 1095 1100

Val Val Leu Leu Asp Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu
1105 1110 1115 1120

Arg Tyr Trp Leu Lys Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe
1125 1130 1135

Gly Asn Pro Val Ala Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg
1140 1145 1150

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<211> 476

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(453)

<223> FRXA00023

<400> 309

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His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser
1 5 10 15

gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca gcc cgt cgc gcc 96
Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala
20 25 30

ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt tca gag caa gtc 144
Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
35 40 45

cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa aca gtc gat gat 192
Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
50 55 60

tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc 240
Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
65 70 75 80

agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac act gtc cgt gaa 288
Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
85 90 95

cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act 336
Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
100 105 110

gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att 384
Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
115 120 125

tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg gcc ttc cac gag 432
Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu

130 135 140 476
 ttg gcg gag gaa ctt aaa cgt tgatcggtttt gcgcattgggt cgc
 Leu Ala Glu Glu Leu Lys Arg
 145 150

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 20 25 30
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
 35 40 45
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
 50 55 60
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
 100 105 110
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
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 130 135 140
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 145 150

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 <223> FRXA02284

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 Met Thr Ser Met Asn
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ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg	163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val	
10 15 20	
cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
25 30 35	
gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
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Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcn nnn	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa	
170 175 180	
nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883

Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr
 250 255 260

ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc 931
 Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg
 265 270 275

gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys
 280 285 290

ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg
 1027
 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp
 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag
 1075
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc
 1123
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg
 1171
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu
 345 350 355

ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg
 1219
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu
 360 365 370

cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt
 1267
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly
 375 380 385

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 1315

Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val
 390 395 400 405

gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa
 1363
 Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu
 410 415 420

aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc
 1411
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe
 425 430 435

aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg
 1459
 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr
 440 445 450

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1507

Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser
455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc
1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro
470 475 480 485

gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc
1603

Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala
490 495 500

gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg
1651

Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro
505 510 515

gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc
1699

Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg
520 525 530

gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag
1747

Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu
535 540 545

att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg
1795

Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu
550 555 560 565

atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac
1843

Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp
570 575 580

ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg
1891

Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu
585 590 595

gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc
1939

Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg
600 605 610

gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct
1987

Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala
615 620 625

gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa
2035

Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys
630 635 640 645

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc
2083

Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu
650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct
2131

Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala
665 670 675

aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc
2179

Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg
680 685 690

gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg
2227

Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp
695 700 705

cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc
2275

Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile
710 715 720 725

gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg
2323

Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val
730 735 740

aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc
2371

Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu
745 750 755

ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag
2419

Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln
760 765 770

ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc
2467

~~Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro~~
775 780 785

tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac
2515

Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His
790 795 800 805

cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc
2563

His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro
810 815 820

cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa
2611

Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu
825 830 835

ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca
2659

Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro
840 845 850

gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc
2707

Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe
855 860 865

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala
890 895 900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc
2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca
3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat
3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca
3124

Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
1000 1005

<210> 312

<211> 1008

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Met Thr Ser Met Asn Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln
 1 5 10 15

Ala Val Asp Lys Val Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser
 20 25 30

Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
 35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
 50 55 60

Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
 65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
 85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
 100 105 110

Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125

Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140

Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160

Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175

Glu Tyr Val Ser Xaa Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190

Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
 195 200 205

Leu Tyr Ile Glu Pro Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
 210 215 220

Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
 225 230 235 240

Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255

Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
 260 265 270

Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285

Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala
 290 295 300

Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr
 305 310 315 320

Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile
 340 345 350
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro
 385 390 395 400
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu
 405 410 415
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala
 420 425 430
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile
 435 440 445
 Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His
 450 455 460
 Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro
 465 470 475 480
 Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln
 485 490 495
 Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu
 500 505 510
 Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu
 515 520 525
 Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala
 530 535 540
 Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val
 545 550 555 560
 Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala
 565 570 575
 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg
 580 585 590
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu
 595 600 605
 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro
 610 615 620
 Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala
 625 630 635 640
 Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala

468

Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
 980 985 990

Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005

<210> 313

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXC02498

<400> 313

caaggtagaa atttgtccgt gggcacttcg tgaaggtgtg atcctcacca ggatcgacaa 60

aggactcgag taacatttac ccggaaagga gttggcgaaa atg agt gaa gag aaa 115
 Met Ser Glu Glu Lys
 1 5

ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc 163
 Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser
 10 15 20

acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211
 Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly
 25 30 35

gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag 259
 Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys
 40 45 50

ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa 307
 Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu
 55 60 65

cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa 355
 Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu
 70 75 80 85

gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt 403
 Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg
 90 95 100

ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa 451
 Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu
 105 110 115

aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca 499
 Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala
 120 125 130

gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat 547

Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp
 135 140 145

gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac 595
 Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn
 150 155 160 165

act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca 643
 Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro
 170 175 180

gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc 691
 Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile
 185 190 195

gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg 739
 Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu
 200 205 210

tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg 787
 Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val
 215 220 225

acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat 835
 Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp
 230 235 240 245

ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc 883
 Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe
 250 255 260

ggg ccg ctg gca atc gtc atg taatttgtcg ttttggggccc ccg 927
 Gly Pro Leu Ala Ile Val Met
 265

<210> 314

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 314

Met Ser Glu Glu Lys Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala
 1 5 10 15

Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser
 20 25 30

Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
 35 40 45

Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
 50 55 60

Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
 65 70 75 80

Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
 85 90 95

Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu

100	105	110
Arg Ile Val Asp Glu Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe		
115	120	125
Pro Val Val Pro Ala Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala		
130	135	140
Glu Lys Asp Ala Asp Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu		
145	150	155
Val Glu Val Asp Asn Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu		
165	170	175
Val Asp Glu Glu Pro Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile		
180	185	190
Ile Met Met Ala Ile Val Gly Val Val Leu Gly Val Val Val Phe Leu		
195	200	205
Gly Phe Glu Met Leu Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val		
210	215	220
Leu Ala Val Gly Val Thr Leu Gly Met Val Gly Ile Ile His Ala Leu		
225	230	235
Arg Thr Ser Arg Asp Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly		
245	250	255
Leu Val Met Thr Phe Gly Pro Leu Ala Ile Val Met		
260	265	

<210> 315

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01491

<400> 315

aacggtgtga aacacattga agtgtcgttg gggtatccgc gcgaatggga gcattggtct 60

gggcagcatg tgtggccata tccagtgatg gaggtggaca atg ctg gat gag tct	115
Met Leu Asp Glu Ser	
1	5

ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct	163
Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala	
10	15
20	

gtt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg	211
Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu	
25	30
35	

gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg	259
Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg	
40	45
50	

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307
 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
 55 60 65
 ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val
 70 75 80 85
 tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403
 Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala
 90 95 100
 cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451
 Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu
 105 110 115
 ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499
 Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile
 120 125 130
 cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547
 Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg
 135 140 145
 ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595
 Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu
 150 155 160 165
 acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643
 Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp
 170 175 180
 gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691
 Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro
 185 190 195
 ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739
 Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala
 200 205 210
 act gca gtg act tgaactggat ggagaggata cct 774
 Thr Ala Val Thr
 215

<210> 316

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

Met Leu Asp Glu Ser Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile
 1 5 10 15

Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
 20 25 30

Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
 35 40 45

Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly
50 55 60

Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu
65 70 75 80

Trp Pro Ser Ser Val Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg
85 90 95

Ala Ala Val Val Ala Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp
100 105 110

Ala Glu Pro Ala Glu Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala
115 120 125

Arg Val Gly Glu Ile Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val
130 135 140

His Cys Ala Asp Arg Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys
145 150 155 160

Ala Trp Phe Pro Leu Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu
165 170 175

Ile Asp Leu Arg Asp Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg
180 185 190

Pro Thr Pro Val Pro Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly
195 200 205

Tyr Val Ile Ala Ala Thr Ala Val Thr
210 215

<210> 317

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1264)

<223> RXA02155

<400> 317

tccggcgtcgc accttaaagt agcgccttaa agcggcgctt caaaccaagc gccctaacca 60

gcaaacacaa caaacacatc taattcagta ggagttccac atg gca gaa aaa ggc 115
Met Ala Glu Lys Gly
1 5

att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163
Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile
10 15 20

aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211
Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro
25 30 35

gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259
Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala

40	45	50	
cct gtg aag gtg agc cga gag aac gtt gct gat ggc cag atc agg gct			307
Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp Gly Gln Ile Arg Ala			
55	60	65	
gtt ttg tac aac gct ggt aat gct aat gcg tgt aat ggt ctg cag ggt			355
Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys Asn Gly Leu Gln Gly			
70	75	80	85
gag aag gat gct cgt gag tct gtt tct cat cta gct caa aat ttg ggc			403
Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu Ala Gln Asn Leu Gly			
	90	95	100
ttg gag gat tcc gat att ggt gtg tgt tcc act ggt ctt att ggt gag			451
Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr Gly Leu Ile Gly Glu			
	105	110	115
ttg ctt ccg atg gat aag ctc aat gca ggt att gat cag ctg acc gct			499
Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile Asp Gln Leu Thr Ala			
	120	125	130
gag ggc gct ttg ggt gac aat ggt gca gct gct gcc aag gcg atc atg			547
Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala Ala Lys Ala Ile Met			
	135	140	145
acc act gac acg gtg gat aag gaa acc gtc gtg ttt gct gat ggt tgg			595
Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val Phe Ala Asp Gly Trp			
	155	160	165
act gtc ggc gga atg ggc aag ggc gtg ggc atg atg gcg ccg tct ctt			643
Thr Val Gly Gly Met Gly Lys Gly Val Gly Met Met Ala Pro Ser Leu			
	170	175	180
gcc acc atg ctg gtc tgc ttg acc act gat gca tcc gtt act cag gaa			691
Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala Ser Val Thr Gln Glu			
	185	190	195
atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc			739
Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr			
	200	205	210
ctg gat att gat gga tca acc tcc aag aat gaa acc gtg ttc ctg ctg			787
Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu			
215	220	225	
gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat			835
Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp			
	235	240	245
gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat			883
Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp			
	250	255	260
gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc			931
Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr			
	265	270	275
aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat			979
Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn			
	280	285	290

ttg ttc aag tgc gca atg ttt gga tct gat cca aac tgg ggt cgc gtg
1027

Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val
295 300 305

ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att
1075

Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile
310 315 320 325

tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct
1123

Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala
330 335 340

cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga
1171

Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg
345 350 355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act
1219

Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr
360 365 370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct
1264

Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser
375 380 385

taaaaagaaa cagcactcca act
1287

<210> 318

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Ala Glu Lys Gly Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala
1 5 10 15

Thr Thr Ala Gly Ile Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val
20 25 30

Val Asn Gln Gly Pro Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn
35 40 45

Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp
50 55 60

Gly Gln Ile Arg Ala Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys
65 70 75 80

Asn Gly Leu Gln Gly Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu
85 90 95

Ala Gln Asn Leu Gly Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr
100 105 110

Gly Leu Ile Gly Glu Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile
 115 120 125
 Asp Gln Leu Thr Ala Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala
 130 135 140
 Ala Lys Ala Ile Met Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val
 145 150 155 160
 Phe Ala Asp Gly Trp Thr Val Gly Gly Met Gly Lys Gly Val Gly Met
 165 170 175
 Met Ala Pro Ser Leu Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala
 180 185 190
 Ser Val Thr Gln Glu Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala
 195 200 205
 Val Thr Phe Asp Thr Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp
 210 215 220
 Thr Val Phe Leu Leu Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln
 225 230 235 240
 Asp Glu Leu Asn Asp Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala
 245 250 255
 Lys Leu Gln Ala Asp Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr
 260 265 270
 Val Val Gly Thr Thr Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr
 275 280 285
 Val Ala Arg Asp Asn Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro
 290 295 300
 Asn Trp Gly Arg Val Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met
 305 310 315 320
 Glu Pro Glu Lys Ile Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu
 325 330 335
 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala
 340 345 350
 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala
 355 360 365
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser
 370 375 380
 Ala Tyr Ser Ser
 385

<210> 319

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA02156

<400> 319

aaccactgac ctgagcttct cctacgtgga gatcaactcc gcgtacagct cttaaaaaga 60

aacagcactc caactaacaa gcagggaaaa gggcacaggc atg aat gac ttg atc 115
 Met Asn Asp Leu Ile
 1 5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
 Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
 10 15 20

cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
 Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
 25 30 35

gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
 Gly Asn Ala Met Val Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
 40 45 50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
 Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
 55 60 65

ggg gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355
 Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
 70 75 80 85

gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
 Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
 90 95 100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
 Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
 105 110 115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
 Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
 120 125 130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547
 Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro
 135 140 145

act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595
 Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
 150 155 160 165

ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
 Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
 170 175 180

gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
 Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
 185 190 195

gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739

Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu
 200 205 210

acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu
 215 220 225

gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu
 230 235 240 245

gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg
 250 255 260

ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser
 265 270 275

gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979
 Val Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu
 280 285 290

ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga
 1027
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg
 295 300 305

aaa gac gac aag gat ggg gaa ctg taaatgagca cgctggaaac ttg
 1074
 Lys Asp Asp Lys Asp Gly Glu Leu
 310 315

<210> 320

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Asn Asp Leu Ile Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val
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Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val
 20 25 30

Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala
 35 40 45

Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro
 50 55 60

Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg
 65 70 75 80

Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro
 85 90 95

Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg
 100 105 110

Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr
115 120 125

Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn
130 135 140

Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn
145 150 155 160

Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro
165 170 175

Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile
180 185 190

Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu
195 200 205

Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro
210 215 220

Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala
225 230 235 240

Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys
245 250 255

Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly
260 265 270

Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile
275 280 285

Gly Thr Met Val Leu Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu
290 295 300

Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu
305 310 315

<210> 321

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN02153

<400> 321

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ccccgcgaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115
Met Ile Met His Asn
1 5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct	211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala	
25 30 35	
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc	259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr	
40 45 50	
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg	307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala	
55 60 65	
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat	355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp	
70 75 80 85	
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt	403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu	
90 95 100	
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt	451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg	
105 110 115	
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag	499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln	
120 125 130	
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct	547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala	
135 140 145	
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt	595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly	
150 155 160 165	
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca	643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro	
170 175 180	
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa	691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys	
185 190 195	
gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg	739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala	
200 205 210	
tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac	787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn	
215 220 225	
ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg	835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val	
230 235 240 245	
ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt	880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu	
250 255 260	
tgaaagaagg cgttaccgca gaa	903

<210> 322

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
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Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu
 20 25 30

Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
 35 40 45

Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
 50 55 60

Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
 65 70 75 80

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
 85 90 95

Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
 100 105 110

Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
 115 120 125

Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
 130 135 140

Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
 145 150 155 160

Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
 245 250 255

Gln Pro His Leu
 260

<210> 323

<211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(880)
 <223> FRXA02153

<400> 323
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 cccccgcaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115
 Met Ile Met His Asn
 1 5
 gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
 10 15 20
 gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211
 Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala
 25 30 35
 tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259
 Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr
 40 45 50
 gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307
 Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala
 55 60 65
 gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355
 Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp
 70 75 80 85
 gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403
 Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu
 90 95 100
 cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451
 Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg
 105 110 115
 ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499
 Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln
 120 125 130
 gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547
 Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala
 135 140 145
 ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595
 Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly
 150 155 160 165
 gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643
 Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro
 170 175 180
 gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa 691

Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys
 185 190 195

gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala
 200 205 210

tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn
 215 220 225

ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val
 230 235 240 245

ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880
 Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu
 250 255 260

tgaaagaagg cgttaccgca gaa 903

<210> 324
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 324
 Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
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Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu
 20 25 30

Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
 35 40 45

Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
 50 55 60

Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
 65 70 75 80

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
 85 90 95

Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
 100 105 110

Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
 115 120 125

Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
 130 135 140

Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
 145 150 155 160

Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
 245 250 255

Gln Pro His Leu
 260

<210> 325
 <211> 414
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(391)
 <223> RXA02154

<400> 325
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caccggttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115
 Leu Lys Glu Gly Val
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu
 40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307
 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly
 55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355
 Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp
 70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401
 Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro
 90 95

ccttaaagcg gcg 414

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<400> 326
Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
 1             5             10             15
Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
          20             25             30
Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
          35             40             45
Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
          50             55             60
Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
 65             70             75             80
Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
          85             90             95
Pro

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<222> (101)..(1273)
<223> RXA02157
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70	75	80	85
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa			403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln			
	90	95	100
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct			451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala			
	105	110	115
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt			499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val			
	120	125	130
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag			547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln			
	135	140	145
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc			595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe			
	150	155	160
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac			643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn			
	170	175	180
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg			691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr			
	185	190	195
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg			739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu			
	200	205	210
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc			787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly			
	215	220	225
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt			835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val			
	230	235	240
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc			883
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile			
	250	255	260
ggg gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc			931
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly			
	265	270	275
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc			979
Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala			
	280	285	290
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc			1027
Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala			

295 300 305
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385
 atc gca taaaggactc aaacttatga ctt
 1296
 Ile Ala
 390
 <210> 328
 <211> 391
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 328
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 20 25 30
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg

115	120	125
Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu 130 135 140		
Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro 145 150 155 160		
Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys 165 170 175		
Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro 180 185 190		
Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys 195 200 205		
Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp 210 215 220		
Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln 225 230 235 240		
His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly 245 250 255		
Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu 260 265 270		
Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val 275 280 285		
Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe 290 295 300		
Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala 305 310 315 320		
Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly 325 330 335		
Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe 340 345 350		

Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu 355 360 365
Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys 370 375 380
Ala Ile Ala Glu Thr Ile Ala 385 390

<210> 329
 <211> 1491
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(1468)

<223> RXS02970

<400> 329

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Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
440 445 450

gcg ttg ttc taagttttct agataacaag gcc
1491

Ala Leu Phe
455

<210> 330

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
 405 410 415
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
 420 425 430
~~Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu~~
~~435 440 445~~
 Leu Thr Phe Ala Gly Ala Leu Phe
 450 455

<210> 331
 <211> 1330
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1330)
 <223> FRXA01009

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	Leu Ala Leu Lys Gly	
	1 5	
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163	
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala		
	10 15 20	
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211	
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe		
	25 30 35	
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259	
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala		
	40 45 50	
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307	
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp		
	55 60 65	
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355	
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg		
	70 75 80 85	
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403	
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn		
	90 95 100	
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451	
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val		
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499	
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly		
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gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547	
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly		
	135 140 145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595	
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly		
	150 155 160 165	
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643	
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr		
	170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691	
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser		
	185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739	
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys		
	200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787	
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala		
	215 220 225	

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc ggc
 1330
 Phe Lys Glu Arg Gly
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<210> 332

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

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 20 25 30
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
 405 410

<210> 333
 <211> 1080
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1057)
 <223> RXA02158

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aaggctattg ccgagacaat cgcataaagg actcaaactt atg act tca caa cca 115
 Met Thr Ser Gln Pro
 1 5

cag gtt cgc cat ttt ctg gct gat gat gat ctc acc cct gca gag cag 163
 Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu Thr Pro Ala Glu Gln
 10 15 20

gca gag gtt ttg acc cta gcc gca aag ctc aag gca gcg ccg ttt tcg 211
 Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys Ala Ala Pro Phe Ser
 25 30 35

gag cgt cca ctc gag gga cca aag tcc gtt gca gtt ctt ttt gat aag 259
 Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala Val Leu Phe Asp Lys
 40 45 50

act tca act cgt act cgc ttc tcc ttc gac gcg ggc atc gct cat ttg 307
 Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala Gly Ile Ala His Leu
 55 60 65

ggg gga cac gcc atc gtc gtg gat tcc ggt agc tca cag atg ggt aag 355
 Gly Gly His Ala Ile Val Val Asp Ser Gly Ser Ser Gln Met Gly Lys
 70 75 80 85

ggc gag tcc ctg cag gac acc gca gct gta ttg tcc cgc tac gtg gaa 403
 Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu Ser Arg Tyr Val Glu
 90 95 100

gca att gtg tgg cgc acc tac gca cac agc aat ttc cac gcc atg gcg 451
 Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn Phe His Ala Met Ala
 105 110 115

gag acg tcc act gtg ccg ctg gtg aac tcc ttg tcc gat gat ctg cac 499
 Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His
 120 125 130

cca tgc cag att ctg gct gat ctg cag act atc gtg gaa aac ctc agc 547
 Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser
 135 140 145

cct gaa gaa ggc cca gca ggc ctt aag ggt aag aag gct gtg tac ctg 595
 Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu
 150 155 160 165

ggc gat ggc gac aac aac atg gcc aac tcc tac atg att ggc ttt gcc 643
 Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr Met Ile Gly Phe Ala
 170 175 180

acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691
 Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro
 185 190 195

cgt gcg gaa ttc gtg gag cgc gcg gaa aag cgt ggc cag gaa acc ggc 739
 Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly
 200 205 210

gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787
 Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu Val Ala Gly Ala Asp
 215 220 225

gtt gtc atc acc gat acc tgg gta tcc atg ggt atg gaa aac gac ggc 835
 Val Val Ile Thr Asp Thr Trp Val Ser Met Gly Met Glu Asn Asp Gly
 230 235 240 245

atc gat cgc acc aca cct ttc gtt cct tac cag gtc aac gat gag gtc 883
 Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val
 250 255 260

atg gcg aaa gct aac gac ggc gcc atc ttc ctg cac tgc ctt cct gcc 931
 Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu His Cys Leu Pro Ala
 265 270 275

tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979
 Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser
 280 285 290

aaa gtt ttc gat gaa gca gaa aac cgc ctc cac gct cag aaa gca ctg
 1027
 Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His Ala Gln Lys Ala Leu
 295 300 305

ctg ctg tgg ctg ctg gcc aac cag ccg agg taagacatgt cccttggtc
 1077
 Leu val Trp Leu Leu Ala Asn Gln Pro Arg
 310 315

aac
 1080

<210> 334

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

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 20 25 30

Ala Ala Pro Phe Ser Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala
 35 40 45

Val Leu Phe Asp Lys Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala
 50 55 60

Gly Ile Ala His Leu Gly Gly His Ala Ile Val Val Asp Ser Gly Ser
 65 70 75 80

Ser Gln Met Gly Lys Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu
 85 90 95

Ser Arg Tyr Val Glu Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn
 100 105 110

Phe His Ala Met Ala Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu
 115 120 125

Ser Asp Asp Leu His Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile
 130 135 140

Val Glu Asn Leu Ser Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys
 145 150 155 160

Lys Ala Val Tyr Leu Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr
 165 170 175

Met Ile Gly Phe Ala Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro
 180 185 190

Glu Gly Phe Gln Pro Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg
 195 200 205

Gly Gln Glu Thr Gly Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu
 210 215 220

Val Ala Gly Ala Asp Val Val Ile Thr Asp Thr Trp Val Ser Met Gly
 225 230 235 240

Met Glu Asn Asp Gly Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln
 245 250 255

Val Asn Asp Glu Val Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu
 260 265 270

His Cys Leu Pro Ala Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile
 275 280 285

Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His
 290 295 300

Ala Gln Lys Ala Leu Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
 305 310 315

<210> 335

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> RXA02160

<400> 335

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                                         Met Thr Asn Arg Ile
                                         1 5

gtt ctt gca tac tcc ggc ggt ctg gac acc act gtg gca att cca tac 163
Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr Val Ala Ile Pro Tyr
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Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu
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ggc cag ggt gga gag aac atg gac aac gtt cgc cag cgt gca ttg gat 259
Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp
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gcc ggt gca gct gag tcc atc gtt gtt gat gca aag gat gag ttc gct 307
Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala Lys Asp Glu Phe Ala
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gag gag tac tgc ctg cca acc atc aag gca aac ggc atg tac atg aag 355
Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn Gly Met Tyr Met Lys
              70              75              80              85

cag tac cca ctg gtt tct gca atc tcc cgc cca ctg atc gtc aag cac 403
Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro Leu Ile Val Lys His
              90              95              100

ctc gtt gag gct ggc aag cag ttc aac ggt acc cac gtt gca cac ggc 451
Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr His Val Ala His Gly
              105              110              115

tgc act ggt aag ggc aac gac cag gtt cgt ttc gag gtc ggc ttc atg 499
Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met
              120              125              130

gac acc gat cca aac ctg gag atc att gca cct gct cgt gac ttc gca 547
Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro Ala Arg Asp Phe Ala
              135              140              145

tgg acc cgc gac aag gct atc gcc ttc gcc gag gag aac aac gtt cca 595

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Ile	Glu	Gln	Ser	Val	Lys	Ser	Pro	Phe	Ser	Ile	Asp	Gln	Asn	Val	Trp	
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Gly	Arg	Ala	Ile	Glu	Thr	Gly	Tyr	Leu	Glu	Asp	Leu	Trp	Asn	Ala	Pro	
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acc	aag	gac	atc	tac	gca	tac	acc	gag	gat	cca	gct	ctg	ggg	aac	gct	739
Thr	Lys	Asp	Ile	Tyr	Ala	Tyr	Thr	Glu	Asp	Pro	Ala	Leu	Gly	Asn	Ala	
		200					205					210				
cca	gat	gag	gtc	atc	atc	tcc	ttc	gag	ggg	ggc	aag	cca	gtc	tcc	atc	787
Pro	Asp	Glu	Val	Ile	Ile	Ser	Phe	Glu	Gly	Gly	Lys	Pro	Val	Ser	Ile	
	215					220					225					
gat	ggc	cgt	cca	gtc	tcc	gta	ctg	cag	gct	att	gaa	gag	ctg	aac	cgt	835
Asp	Gly	Arg	Pro	Val	Ser	Val	Leu	Gln	Ala	Ile	Glu	Glu	Leu	Asn	Arg	
230					235					240					245	
cgt	gca	ggc	gca	cag	ggc	gtt	ggc	cgc	ctt	gac	atg	gtt	gag	gac	cgt	883
Arg	Ala	Gly	Ala	Gln	Gly	Val	Gly	Arg	Leu	Asp	Met	Val	Glu	Asp	Arg	
				250					255					260		
ctc	gtg	ggc	atc	aag	tcc	cgc	gaa	atc	tac	gaa	gca	cca	ggc	gca	atc	931
Leu	Val	Gly	Ile	Lys	Ser	Arg	Glu	Ile	Tyr	Glu	Ala	Pro	Gly	Ala	Ile	
			265					270						275		
gca	ctg	att	aag	gct	cac	gag	gct	ttg	gaa	gat	gtc	acc	atc	gag	cgc	979
Ala	Leu	Ile	Lys	Ala	His	Glu	Ala	Leu	Glu	Asp	Val	Thr	Ile	Glu	Arg	
		280					285					290				
gaa	ctg	gct	cgc	tac	aag	cgc	ggc	gtt	gac	gca	cgt	tgg	gct	gag	gaa	
1027																
Glu	Leu	Ala	Arg	Tyr	Lys	Arg	Gly	Val	Asp	Ala	Arg	Trp	Ala	Glu	Glu	
	295					300					305					
gta	tac	gac	ggc	ctg	tgg	ttc	gga	cct	ctg	aag	cgc	tcc	ctg	gac	gcg	
1075																
Val	Tyr	Asp	Gly	Leu	Trp	Phe	Gly	Pro	Leu	Lys	Arg	Ser	Leu	Asp	Ala	
310					315					320					325	
ttc	att	gat	tcc	acc	cag	gag	cac	gtc	acc	ggc	gat	atc	cgc	atg	gtt	
1123																
Phe	Ile	Asp	Ser	Thr	Gln	Glu	His	Val	Thr	Gly	Asp	Ile	Arg	Met	Val	
				330						335				340		
ctg	cac	gca	ggg	tcc	atc	acc	atc	aat	ggg	cgt	cgt	tcc	agc	cac	tcc	
1171																
Leu	His	Ala	Gly	Ser	Ile	Thr	Ile	Asn	Gly	Arg	Arg	Ser	Ser	His	Ser	
			345					350					355			
ctg	tac	gac	ttc	aac	ctg	gct	acc	tac	gac	acc	ggc	gac	acc	ttc	gac	
1219																
Leu	Tyr	Asp	Phe	Asn	Leu	Ala	Thr	Tyr	Asp	Thr	Gly	Asp	Thr	Phe	Asp	
		360					365					370				

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag
1267

Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys
375 380 385

atc gct aac aag cgc gat cgc gaa gct ggc aac aac taagccacct
1313

Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn Asn
390 395 400

tttcaagcat cca
1326

<210> 336

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

Met Thr Asn Arg Ile Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr
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20 25 30

Val Ser Leu Asp Leu Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg
35 40 45

Gln Arg Ala Leu Asp Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala
50 55 60

Lys Asp Glu Phe Ala Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn
65 70 75 80

Gly Met Tyr Met Lys Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro
85 90 95

Leu Ile Val Lys His Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr
100 105 110

His Val Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe
115 120 125

Glu Val Gly Phe Met Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro
130 135 140

Ala Arg Asp Phe Ala Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu
145 150 155 160

Glu Asn Asn Val Pro Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile
165 170 175

Asp Gln Asn Val Trp Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp
180 185 190

Leu Trp Asn Ala Pro Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro
195 200 205

Ala Leu Gly Asn Ala Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly
210 215 220

Lys Pro Val Ser Ile Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile
 225 230 235 240
 Glu Glu Leu Asn Arg Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp
 245 250 255
 Met Val Glu Asp Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu
 260 265 270
 Ala Pro Gly Ala Ile Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp
 275 280 285
 Val Thr Ile Glu Arg Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala
 290 295 300
 Arg Trp Ala Glu Glu Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys
 305 310 315 320
 Arg Ser Leu Asp Ala Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly
 325 330 335
 Asp Ile Arg Met Val Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg
 340 345 350
 Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr
 355 360 365
 Gly Asp Thr Phe Asp Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His
 370 375 380
 Gly Leu Ser Ser Lys Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn
 385 390 395 400
 Asn

<210> 337
 <211> 1554
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1531)
 <223> RXN02162

<400> 337
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 gactagaact tcaagtattt agaaagtaga agaacaccac atg gaa cag cac gga 115
 Met Glu Gln His Gly
 1 5
 acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser
 10 15 20
 gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211
 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu

25	30	35	
gcc cct tat gat gtg ttg gcc tcc aag gca cac gcc aag gtt ttg cac Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His Ala Lys Val Leu His 40 45 50			259
caa gca gat cta ctt tct gat gaa gat cta gcc acc atg ctg gct ggg Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala Thr Met Leu Ala Gly 55 60 65			307
ctt gat cag ctg ggc aag gat gtc gcc gac gga acc ttc ggt ccg ctg Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly Thr Phe Gly Pro Leu 70 75 80 85			355
cct tct gat gag gat gtg cac ggc gcg atg gaa cgc ggt gtg att gac Pro Ser Asp Glu Asp Val His Gly Ala Met Glu Arg Gly Val Ile Asp 90 95 100			403
cgc gtt ggt cct gag gtg ggc ggc cgt ctg cgc gct ggt cgt tcc cgc Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg Ala Gly Arg Ser Arg 105 110 115			451
aac gac cag gtg gca acc ctg ttc cgc atg tgg gtc cgc gac gca gtg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp Val Arg Asp Ala Val 120 125 130			499
cgc gac atc gcg ctg gga aca acc gag ctt gtc gac gcc ctc agc gcc Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val Asp Ala Leu Ser Ala 135 140 145			547
caa gct aag gca cat gca ggc gcg atc atg cca ggc aag acc cac ttc Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro Gly Lys Thr His Phe 150 155 160 165			595
cag gca gct cag ccg gtc ctt ctg gca cac cag ctg ctg gca cac gca Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln Leu Leu Ala His Ala 170 175 180			643
cag cct ttg ctg cgc gat att gat cgt atc cgt gac ctg gac aag cgt Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg Asp Leu Asp Lys Arg 185 190 195			691
ctt gcg gtg tct cct tac ggt tcc ggc gca ctt gct ggt tcc tct ttg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu Ala Gly Ser Ser Leu 200 205 210			739
aag ctc aac cct gaa gca atc gct gaa gaa ctc ggc ttt gat tcc gca Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu Gly Phe Asp Ser Ala 215 220 225			787
gca gat aac tcc att gat gcc acc agc tcc cgc gat ttc gca tct gaa Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg Asp Phe Ala Ser Glu 230 235 240 245			835
acc gcc ttc gtg ctg gcg cag ctt gca gtg gat atg tcc cgc ttg gct Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp Met Ser Arg Leu Ala 250 255 260			883
gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu 265 270 275			931

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tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 979
Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn
      280                      285                      290

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt
1027
Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly
      295                      300                      305

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac
1075
Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
310                      315                      320                      325

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg
1123
Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
      330                      335                      340

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg
1171
Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
      345                      350                      355

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc
1219
Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
      360                      365                      370

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc
1267
Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
      375                      380                      385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc
1315
Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
390                      395                      400                      405

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt
1363
Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
      410                      415                      420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt
1411
Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
      425                      430                      435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt
1459
Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
      440                      445                      450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag
1507
Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
      455                      460                      465

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tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg
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 Trp Ala Arg Ala Gly Val Arg Arg
 470 475

<210> 338

<211> 477

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe
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Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
 20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
 85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
 100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
 130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
 145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
 165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
 180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
 195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
 210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
 225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp
 245 250 255

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe

260	265	270
Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met		
275	280	285
Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser		
290	295	300
Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala		
305	310	315
Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile		
325	330	335
Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly		
340	345	350
Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala		
355	360	365
Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg		
370	375	380
Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val		
385	390	395
Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu		
405	410	415
Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val		
420	425	430
Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr		
435	440	445
Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser		
450	455	460
Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg		
465	470	475

<210> 339

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> FRXA02161

<400> 339

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gactagaact tcaagtatttt agaaagtaga agaacaccac atg gaa cag cac gga	115
Met Glu Gln His Gly	
1	5

acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc	163
Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser	

10	15	20	
gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg			211
Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu			
25	30	35	
gcc cct tat gat gtg ttg gcc tcc aag gca cac gcc aag gtt ttg cac			259
Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His Ala Lys Val Leu His			
40	45	50	
caa gca gat cta ctt tct gat gaa gat cta gcc acc atg ctg gct ggg			307
Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala Thr Met Leu Ala Gly			
55	60	65	
ctt gat cag ctg ggc aag gat gtc gcc gac gga acc ttc ggt ccg ctg			355
Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly Thr Phe Gly Pro Leu			
70	75	80	85
cct tct gat gag gat gtg cac ggc gcg atg gaa cgc ggt gtg att gac			403
Pro Ser Asp Glu Asp Val His Gly Ala Met Glu Arg Gly Val Ile Asp			
90	95	100	
cgc gtt ggt cct gag gtg ggc ggc cgt ctg cgc gct ggt cgt tcc cgc			451
Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg Ala Gly Arg Ser Arg			
105	110	115	
aac gac cag gtg gca acc ctg ttc cgc atg tgg gtc cgc gac gca gtg			499
Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp Val Arg Asp Ala Val			
120	125	130	
cgc gac atc gcg ctg gga aca acc gag ctt gtc gac gcc ctc agc gcc			547
Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val Asp Ala Leu Ser Ala			
135	140	145	
caa gct aag gca cat gca ggc gcg atc atg cca ggc aag acc cac ttc			595
Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro Gly Lys Thr His Phe			
150	155	160	165
cag gca gct cag ccg gtc ctt ctg gca cac cag ctg ctg gca cac gca			643
Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln Leu Leu Ala His Ala			
170	175	180	
cag cct ttg ctg cgc gat att gat cgt atc cgt gac ctg gac aag cgt			691
Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg Asp Leu Asp Lys Arg			
185	190	195	
ctt gcg gtg tct cct tac ggt tcc ggc gca ctt gct ggt tcc tct ttg			739
Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu Ala Gly Ser Ser Leu			
200	205	210	
aag ctc aac cct gaa gca atc gct gaa gaa ctc ggc ttt gat tcc gca			787
Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu Gly Phe Asp Ser Ala			
215	220	225	
gca gat aac tcc att gat gcc acc agc tcc cgc gat ttc gca tct gaa			835
Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg Asp Phe Ala Ser Glu			
230	235	240	245
acc gcc ttc gtg ctg gcg cag ctt gca ngc gga tat gtc ccg ctt gcc			883
Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly Tyr Val Pro Leu Gly			
250	255	260	

tgaagaaatc atcgcatggt gca

906

<210> 340

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe
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Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
 20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
 85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
 100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
 130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
 145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
 165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
 180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
 195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
 210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
 225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly
 245 250 255

Tyr Val Pro Leu Gly
 260

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<220>  
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<222> (101)..(763)  
<223> FRXA02162
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509

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 185 190 195

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
 200 205 210

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 786
 Trp Ala Arg Ala Gly Val Arg Arg
 215 220

<210> 342

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe
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Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met
 20 25 30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser
 35 40 45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala
 50 55 60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile
 65 70 75 80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly
 85 90 95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala
 100 105 110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg
 115 120 125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val
 130 135 140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu
 145 150 155 160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val
 165 170 175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr
 180 185 190

Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser
 195 200 205

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg
 210 215 220

<210> 343
 <211> 1269
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1246)
 <223> RXA02262

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 Met Thr Ala Thr Tyr
 1 5
 acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
 Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
 10 15 20
 atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
 Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
 25 30 35
 gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
 Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
 40 45 50
 aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
 Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
 55 60 65
 ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
 Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
 70 75 80 85
 ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
 Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
 90 95 100
 gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451
 Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His
 105 110 115
 acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499
 Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met
 120 125 130
 tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547
 Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val
 135 140 145
 ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595
 Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val
 150 155 160 165
 gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643
 Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu

	170	175	180	
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc				691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly				
	185	190	195	
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa				739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu				
	200	205	210	
gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc				787
Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile				
	215	220	225	
gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca				835
Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro				
	230	235	240	245
tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca				883
Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro				
	250	255	260	
gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc				931
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu				
	265	270	275	
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc				979
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly				
	280	285	290	
cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac				
1027				
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp				
	295	300	305	
ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc				
1075				
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly				
	310	315	320	325
gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc				
1123				
Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile				
	330	335	340	
atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca				
1171				
Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala				
	345	350	355	
acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg				
1219				
Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu				
	360	365	370	
aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg				
1266				
Asn Leu Trp Glu Ser Pro Ala Leu Ala				
	375	380		

aaa
1269

<210> 344
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 344

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Met Thr Ala Thr Tyr Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu
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Ser Glu Pro Asp Met Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys
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Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr
  35          40          45

Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
  50          55          60

Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
  65          70          75          80

Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
          85          90          95

Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
          100         105         110

Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
          115         120         125

Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
          130         135         140

Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
          145         150         155         160

Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
          165         170         175

Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
          180         185         190

Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
          195         200         205

Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
          210         215         220

Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
          225         230         235         240

Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
          245         250         255

Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
          260         265         270

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Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285

Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300

Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320

Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335

Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
 340 345 350

Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
 355 360 365

Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
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<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA00219

<400> 345

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cacaagcact aaaacagcat taaagaaaga aagctttttc gtg gcc cgt aag aaa 115
 Val Ala Arg Lys Lys
 1 5

aac acg tcc gat caa tcc cgc tcc caa gct gcc aac acg ccc att gct 163
 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala
 10 15 20

ggc acc tat gag ggt gaa tat tcc gtc atc gag ttg gag gcc gat tcc 211
 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser
 25 30 35

tac acc acc gat ggc tgg ttg atc agc att aat ggc gtg ccc agc tct 259
 Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser
 40 45 50

cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg 307
 His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg
 55 60 65

tgg atc gct acc ggc gct cgg gcg ttc atc gat gcg cat cag gat gca 355
 Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala
 70 75 80 85

tcc aag ctg cgg att act cac ctc ggc ggc ggt gcg tgc acg atg gcc 403
 Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly Ala Cys Thr Met Ala

	90	95	100	
agg tat ttc gcg gat gtt tac ccg cag tca cgc aac act gtc gtg gaa				451
Arg Tyr Phe Ala Asp Val Tyr Pro Gln Ser Arg Asn Thr Val Val Glu				
	105	110	115	
ttg gat gca gag ctt gcc cgc ctg tcg cgt gaa tgg ttc gac att ccg				499
Leu Asp Ala Glu Leu Ala Arg Leu Ser Arg Glu Trp Phe Asp Ile Pro				
	120	125	130	
cgc gcg cca cgg gta aag att cgt gtg gat gat gcc cga atg gtg gca				547
Arg Ala Pro Arg Val Lys Ile Arg Val Asp Asp Ala Arg Met Val Ala				
	135	140	145	
gaa tct ttc act ccc gca agc cgc gat gtg atc atc cgt gac gtt ttt				595
Glu Ser Phe Thr Pro Ala Ser Arg Asp Val Ile Ile Arg Asp Val Phe				
	150	155	160	165
gcc gga gct atc acg ccg cag aac ttc acc acc gtg gag ttc ttt gag				643
Ala Gly Ala Ile Thr Pro Gln Asn Phe Thr Thr Val Glu Phe Phe Glu				
	170	175	180	
cac tgt cac cgt ggc ctt gct ccc ggc gga ttg tac gtt gcc aac tgt				691
His Cys His Arg Gly Leu Ala Pro Gly Gly Leu Tyr Val Ala Asn Cys				
	185	190	195	
ggc gat cat tcg gat ctg cgc gga gct aaa tct gag ctc gcg gga atg				739
Gly Asp His Ser Asp Leu Arg Gly Ala Lys Ser Glu Leu Ala Gly Met				
	200	205	210	
atg gag gtg ttc gag cac gtc gcg gtc atc gcc gat ccc ccg atg ctt				787
Met Glu Val Phe Glu His Val Ala Val Ile Ala Asp Pro Pro Met Leu				
	215	220	225	
aaa ggg cgc cgt tac ggc aac atc att ttg atg ggt tca gac acc gag				835
Lys Gly Arg Arg Tyr Gly Asn Ile Ile Leu Met Gly Ser Asp Thr Glu				
	230	235	240	245
ttc ttt agc tcc aac agc acg gaa gcg tcc gcg att acc cgt gag ctt				883
Phe Phe Ser Ser Asn Ser Thr Glu Ala Ser Ala Ile Thr Arg Glu Leu				
	250	255	260	
ctt ggc ggc ggc gtt cca gcg cag tac aag gat gaa tcc tgg gtg cgg				931
Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp Glu Ser Trp Val Arg				
	265	270	275	
aaa ttc gcc tcg gga gcc cag gcc cgc cac gat ggg gtc tct acc ctc				979
Lys Phe Ala Ser Gly Ala Gln Ala Arg His Asp Gly Val Ser Thr Leu				
	280	285	290	
caa atg ccg agt gat act cca caa cac cct gcg gaa acg ccg gag cat				
1027				
Gln Met Pro Ser Asp Thr Pro Gln His Pro Ala Glu Thr Pro Glu His				
	295	300	305	
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1065				
Ser Asn Thr Gln Pro				
310				

<210> 346

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Val Ala Arg Lys Lys Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala
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 20 25 30

Leu Glu Ala Asp Ser Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn
 35 40 45

Gly Val Pro Ser Ser His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu
 50 55 60

Phe Glu Tyr Met Arg Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp
 65 70 75 80

Ala His Gln Asp Ala Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly
 85 90 95

Ala Cys Thr Met Ala Arg Tyr Phe Ala Asp Val Tyr Pro Gln Ser Arg
 100 105 110

Asn Thr Val Val Glu Leu Asp Ala Glu Leu Ala Arg Leu Ser Arg Glu
 115 120 125

Trp Phe Asp Ile Pro Arg Ala Pro Arg Val Lys Ile Arg Val Asp Asp
 130 135 140

Ala Arg Met Val Ala Glu Ser Phe Thr Pro Ala Ser Arg Asp Val Ile
 145 150 155 160

Ile Arg Asp Val Phe Ala Gly Ala Ile Thr Pro Gln Asn Phe Thr Thr
 165 170 175

Val Glu Phe Phe Glu His Cys His Arg Gly Leu Ala Pro Gly Gly Leu
 180 185 190

~~Tyr Val Ala Asn Cys Gly Asp His Ser Asp Leu Arg Gly Ala Lys Ser~~
 195 200 205

Glu Leu Ala Gly Met Met Glu Val Phe Glu His Val Ala Val Ile Ala
 210 215 220

Asp Pro Pro Met Leu Lys Gly Arg Arg Tyr Gly Asn Ile Ile Leu Met
 225 230 235 240

Gly Ser Asp Thr Glu Phe Phe Ser Ser Asn Ser Thr Glu Ala Ser Ala
 245 250 255

Ile Thr Arg Glu Leu Leu Gly Gly Gly Val Pro Ala Gln Tyr Lys Asp
 260 265 270

Glu Ser Trp Val Arg Lys Phe Ala Ser Gly Ala Gln Ala Arg His Asp
 275 280 285

Gly Val Ser Thr Leu Gln Met Pro Ser Asp Thr Pro Gln His Pro Ala

290

295

300

Glu Thr Pro Glu His Ser Asn Thr Gln Pro
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<210> 347

<211> 1662

<212> DNA

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<220>

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<222> (101)..(1639)

<223> RXA01508

<400> 347

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ccgccgtcat cttgatcgtg gtgggaaccg taaacgctgc atg tct gat tta gga 115
Met Ser Asp Leu Gly
1 5

ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala
10 15 20

tcg ggg ctg gtc tat gag cta gcc ctg gta tcg ctt tcc acc agc ttg 211
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu
25 30 35

aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val
40 45 50

gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp
55 60 65

cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly
70 75 80 85

ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln
90 95 100

tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val
105 110 115

ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu
120 125 130

gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct 547
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala
135 140 145

gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
	310	315	320	325
atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
	1267			

Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu
 375 380 385

ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg
 1315

Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val
 390 395 400 405

gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt
 1363

Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val
 410 415 420

gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac
 1411

Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His
 425 430 435

gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct
 1459

Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro
 440 445 450

gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc
 1507

Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe
 455 460 465

ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat
 1555

Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn
 470 475 480 485

cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg
 1603

Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val
 490 495 500

gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac
 1649

Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp
 505 510

gatgcgctgt gtg
 1662

<210> 348

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

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 20 25 30

Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile
 35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys
 50 55 60
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu
 65 70 75 80
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe
 85 90 95
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala
 100 105 110
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile
 115 120 125
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala
 130 135 140
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala
 145 150 155 160
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala
 165 170 175
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val
 180 185 190
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val
 195 200 205
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser
 210 215 220
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val
 225 230 235 240
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg
 245 250 255
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr
 260 265 270
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn
 275 280 285
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala
 290 295 300
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu
 305 310 315 320
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp
 325 330 335
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp
 340 345 350
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp
 355 360 365

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg
 370 375 380

Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu
 385 390 395 400

Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp
 405 410 415

Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln
 420 425 430

Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe
 435 440 445

Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr
 450 455 460

Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val
 465 470 475 480

Phe Gly Leu Asp Asn Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp
 485 490 495

His Pro Arg Val Val Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly
 500 505 510

Asp

<210> 349

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXA01757

<400> 349

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gtaaaccacg tttccgtatt gtcttgagc cgaattcata atg cca aca gca agc 115
 Met Pro Thr Ala Ser
 1 5

cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile
 10 15 20

gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211
 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu
 25 30 35

gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp
 40 45 50

ttg ttc ctg gac ctc ggc gca aca tgg ttc tgg ctc aac gaa cca ctt 307

Leu	Phe	Leu	Asp	Leu	Gly	Ala	Thr	Trp	Phe	Trp	Leu	Asn	Glu	Pro	Leu	
55						60					65					
gtg	cag	caa	ctc	gtc	aat	aat	ctc	ggc	ctc	ggc	aca	ttc	cct	cag	gcc	355
Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	
70					75					80					85	
atc	gag	ggt	gat	gcg	ctt	ttt	gag	acg	ctt	gtc	gac	gcc	ccg	agc	cgc	403
Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	
				90					95					100		
ctg	cgg	ggt	aac	ccc	ata	gac	gct	gct	tca	ggc	agg	ttc	caa	gca	ggg	451
Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	
			105					110					115			
gcc	tcc	tcg	ctt	gcg	ctc	ggg	ctt	gca	gcc	cag	ctc	aag	cca	gga	gtt	499
Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	
			120				125					130				
tta	gaa	ctc	ggg	gac	ccc	gtc	cat	tct	ctc	agt	gag	gaa	gat	ggg	gaa	547
Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	
	135					140					145					
atc	gtt	gtg	aag	tct	tcc	aaa	cag	att	gtg	agg	gca	aag	cac	gtc	atc	595
Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	
150					155					160					165	
att	gcg	gtt	cca	ccg	gca	ctc	gct	gcc	gag	ttg	att	ggt	ttc	acc	cta	643
Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	
				170					175					180		
gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	
			185					190					195			
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	
		200					205					210				
tcg	gct	ggg	ggt	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	
	215					220					225					
ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggt	gga	835
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	
230					235					240				245		
cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	
				250					255					260		
gga	ttt	aat	cta	aaa	tct	taa	acctcgt	attttccctg	ata							924
Gly	Phe	Asn	Leu	Lys	Ser											
			265													
<210>	350															
<211>	267															
<212>	PRT															
<213>	Corynebacterium glutamicum															

<400> 350

Met Pro Thr Ala Ser Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly
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Ile Ser Gly Leu Ile Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn
 20 25 30

Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser
 35 40 45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp
 50 55 60

Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly
 65 70 75 80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val
 85 90 95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly
 100 105 110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln
 115 120 125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser
 130 135 140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg
 145 150 155 160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu
 165 170 175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His
 180 185 190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu
 195 200 205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln
 210 215 220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala
 225 230 235 240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln
 245 250 255

Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser
 260 265

<210> 351

<211> 636

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(613)

<400> 351

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acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163

caa gct ctc att ttg cag att ttg qac aaa caa aaa gtc acc agc cag 211

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259

gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355

gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403

gat qaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451

cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595

ctc agc ggc cgc acc act taaagcgccc ctaqttcaag gct 636

<210> 352

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val

1	5	10	15
Thr Arg Thr	Ala Arg Gln Ala	Leu Ile Leu Gln Ile	Leu Asp Lys Gln
	20	25	30
Lys Val Thr	Ser Gln Val Gln	Leu Ser Glu Leu	Leu Leu Asp Glu Gly
	35	40	45
Ile Asp Ile	Thr Gln Ala Thr	Leu Ser Arg Asp	Leu Asp Glu Leu Gly
	50	55	60
Ala Arg Lys	Val Arg Pro Asp	Gly Gly Arg Ala	Tyr Tyr Ala Val Gly
	65	70	75
Pro Val Asp	Ser Ile Ala Arg	Glu Asp Leu Arg	Gly Pro Ser Glu Lys
	85	90	95
Leu Arg Arg	Met Leu Asp Glu	Leu Leu Val Ser	Thr Asp His Ser Gly
	100	105	110
Asn Ile Ala	Met Leu Arg Thr	Pro Pro Gly Ala	Ala Gln Tyr Leu Ala
	115	120	125
Ser Phe Ile	Asp Arg Val Gly	Leu Lys Glu Val	Val Gly Thr Ile Ala
	130	135	140
Gly Asp Asp	Thr Val Phe Val	Leu Ala Arg Asp	Pro Leu Thr Gly Lys
	145	150	155
Glu Leu Gly	Glu Leu Leu Ser	Gly Arg Thr Thr	
	165	170	

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(391)
 <223> RXN02154

<400> 353
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 caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115
 Leu Lys Glu Gly Val
 1 5
 acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu
 10 15 20
 acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala
 25 30 35
 gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu
 40 45 50

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg 163
 Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu
 10 15 20

gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc 211
 Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile
 25 30 35

ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac 259
 Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr
 40 45 50

caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct 307
 Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala
 55 60 65

acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag 355
 Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu
 70 75 80 85

tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc 403
 Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu
 90 95 100

gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa 451
 Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu
 105 110 115

atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca 499
 Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala
 120 125 130

ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc 547
 Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe
 135 140 145

tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc 595
 Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val
 150 155 160 165

aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct 643
 Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser
 170 175 180

gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc 691
 Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr
 185 190 195

gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc 739
 Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe
 200 205 210

tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc 787
 Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe
 215 220 225

gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc 835
 Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly
 230 235 240 245

cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa 883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc
 1027

His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc
 1075

Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc
 1123

Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171

Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca
 1219

Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267

Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
 375 380 385

aag aaa ggc gca taaataacat gccaaagcgt tca

1382
 Lys Lys Gly Ala
 390

<210> 356
 <211> 393
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 356
 Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser
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Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe
 20 25 30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr
 35 40 45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50 55 60
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala
 385 390

<210> 357

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXS00905

<400> 357

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tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115
 Met Thr Gln Phe Glu
 1 5

aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
 10 15 20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
 25 30 35

cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu
 40 45 50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp
 55 60 65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro
 70 75 80 85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu
 90 95 100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly
 105 110 115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn
 120 125 130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp
 135 140 145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595

Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly
 150 155 160 165
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp
 170 175 180
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr
 185 190 195
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr
 200 205 210
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala
 215 220 225
 gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg
 230 235 240 245
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys
 250 255 260
 ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924
 Leu Glu Gly Arg Ala Leu
 265

<210> 358

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn
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 Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn
 20 25 30
 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys
 35 40 45
 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu
 50 55 60
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly
 65 70 75 80
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val
 85 90 95
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr
 100 105 110
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val
130 135 140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly
145 150 155 160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys
165 170 175

Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn
180 185 190

Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly
195 200 205

Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly
210 215 220

Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val
225 230 235 240

Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys
245 250 255

Gln His His Arg Lys Leu Glu Gly Arg Ala Leu
260 265

<210> 359

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXS00906

<400> 359

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gctgttgatg ctctcgtcgc ccttctggat actttgcgcg atg aac acg gac gca 115

Met Asn Thr Asp Ala
1 5

ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163
Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro
10 15 20

tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211
Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val
25 30 35

gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259
Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg
40 45 50

cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307
Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala
55 60 65

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ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355
Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val
70 75 80 85

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403
Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His
90 95 100

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451
Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp
105 110 115

gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499
Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser
120 125 130

acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547
Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val
135 140 145

acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595
Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu
150 155 160 165

gtc aac cca taagcagaat tggcactcta cgg 627
Val Asn Pro

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<210> 360

<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

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Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn
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Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly
20 25 30

Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser
35 40 45

Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr
50 55 60

Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys
65 70 75 80

Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu
85 90 95

Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile
100 105 110

Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr
115 120 125

Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

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130 135 140

Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys
 145 150 155 160

Thr Glu Leu Ile Glu Val Asn Pro
 165

<210> 361
 <211> 246
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(223)
 <223> RXS00907

<400> 361
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actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115
 Leu Ala Leu Tyr Gly
 1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
 10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
 25 30 35

aac tac acc aag tagacccaaa agcaggcggtt aac 246
 Asn Tyr Thr Lys
 40

<210> 362
 <211> 41
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 362
 Leu Ala Leu Tyr Gly Val Glu Glu Pro Leu Thr Val Ile His Ser Ala
 1 5 10 15

Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu
 20 25 30

Ala Leu Phe Leu Leu Asn Tyr Thr Lys
 35 40

<210> 363
 <211> 1281
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXS02001

<400> 363

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gatagtcacag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115
 Met Pro Val Ile Asn
 1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
 Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
 10 15 20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
 His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
 25 30 35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
 Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
 40 45 50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
 Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
 55 60 65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
 Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
 70 75 80 85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403
 Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
 90 95 100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
 Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
 105 110 115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
 Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
 120 125 130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547
 Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
 135 140 145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
 Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
 150 155 160 165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
 Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
 170 175 180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
 Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
 185 190 195

ggg gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
 Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

200	205	210	
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val 215 220 225			787
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp 230 235 240 245			835
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe 250 255 260			883
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val 265 270 275			931
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn 280 285 290			979
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct 1027 Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala 295 300 305			
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg 1075 Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser 310 315 320 325			
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg 1123 Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro 330 335 340			
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac 1171 Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn 345 350 355			
ccc gcc tat att ttc aac gac gag gac ggc ccc tac ggc gca tcg ttc 1219 Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe 360 365 370			
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg 1268 Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly 375 380 385			
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<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

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Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val
 20 25 30

Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp
 35 40 45

Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
 50 55 60

Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala
 65 70 75 80

Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro
 85 90 95

Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu
 100 105 110

Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val
 115 120 125

Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val
 130 135 140

Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr
 145 150 155 160

Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr
 165 170 175

Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr
 180 185 190

Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile
 195 200 205

Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg
 210 215 220

Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His
 225 230 235 240

Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly
 245 250 255

Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg
 260 265 270

Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala
 275 280 285

Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala
 290 295 300

Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val
 305 310 315 320

Asn Pro Asn Gly Ser Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe
325 330 335

Leu Glu Lys Arg Pro Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser
340 345 350

Ala Gly Leu His Asn Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro
355 360 365

Tyr Gly Ala Ser Phe Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu
370 375 380

Lys Gly
385

<210> 365

<211> 1386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1363)

<223> RXS02101

<400> 365

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agtttttagtg tcgctgcgca ggtactctac tatctaatacc atg agc cgc att tca 115
Met Ser Arg Ile Ser
1 5

gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca 163
Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser Trp Gln Glu Ala Ala
10 15 20

tat cag gat ttc cac gaa cat cct gag ctc tcc ggc ttc gaa tca gag 211
Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser Gly Phe Glu Ser Glu
25 30 35

acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg 259
~~Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg Phe Asp Cys Glu Val~~
40 45 50

att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg 307
Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala Val Phe Arg Asn Gly
55 60 65

tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat 355
Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met Arg Ala Asp Phe Asp
70 75 80 85

ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt 403
Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro Phe Ala Ser Thr Arg
90 95 100

atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly
105 110 115

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat 499
 His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp
 120 125 130

gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca 547
 Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro
 135 140 145

tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta 595
 Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu
 150 155 160 165

gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc 643
 Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val
 170 175 180

ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct 691
 Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala
 185 190 195

gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt 739
 Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly
 200 205 210

tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att 787
 Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile
 215 220 225

gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat 835
 Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp
 230 235 240 245

ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac 883
 Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn
 250 255 260

acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac 931
 Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn
 265 270 275

gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt 979
 Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg
 280 285 290

ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac
 1027
 Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr
 295 300 305

ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act
 1075
 Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr
 310 315 320 325

gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct
 1123
 Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala
 330 335 340

tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc
 1171

Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe
345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag
1219

Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln
360 365 370

tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc
1267

Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala
375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct
1315

Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala
390 395 400 405

gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac
1363

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410 415 420

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1386

<210> 366

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

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Trp Gln Glu Ala Ala Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser
20 25 30

Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg
35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala
50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met
65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro
85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val
100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala
115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile
130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

145						150						155						160
Val	Ala	Gly	Gly	Leu	Val	Asp	Leu	Ile	Pro	Arg	Pro	Asp	Val	Cys	Phe			
				165					170					175				
Gly	Gln	His	Val	Val	Pro	Gly	Ala	Ala	Gly	Thr	Val	Met	Ser	Met	Pro			
				180					185					190				
Gly	Gly	Ala	Leu	Ala	Ala	Cys	Asp	Ser	Ile	Glu	Ile	Arg	Ile	Gln	Gly			
				195					200					205				
Arg	Ser	Ala	His	Gly	Ser	Met	Pro	His	Asn	Ser	Ile	Asp	Pro	Thr	Tyr			
				210					215					220				
Val	Ala	Ala	Met	Ile	Val	Val	Arg	Leu	Gln	Gly	Ile	Val	Gly	Arg	Glu			
225					230					235					240			
Val	Ser	Pro	Glu	Asp	Phe	Ala	Val	Ile	Ser	Val	Gly	Thr	Leu	Gln	Ser			
				245					250					255				
Gly	Asn	Thr	Asn	Asn	Thr	Ile	Pro	Ala	Ser	Ala	Arg	Leu	Val	Leu	Asn			
				260					265					270				
Cys	Arg	Phe	Tyr	Asn	Asp	Lys	Val	Lys	His	Lys	Val	Tyr	Arg	Ala	Ile			
				275					280					285				
Glu	Arg	Val	Val	Arg	Gly	Glu	Cys	Leu	Ala	Ser	Gly	Ile	Glu	Glu	Glu			
				290					295					300				
Pro	Val	Ile	Glu	Tyr	Phe	Ala	His	Gly	Asp	Leu	Thr	Asn	Asn	Thr	Pro			
305					310					315					320			
Val	Val	Phe	Asp	Thr	Val	Arg	Pro	Val	Phe	Asp	Asp	Val	Phe	Gly	Glu			
				325					330					335				
Asp	Ser	Ile	Asp	Ala	Tyr	Arg	Trp	Thr	Ala	Ser	Glu	Asp	Phe	Pro	Ser			
				340					345					350				
Ile	Pro	Lys	Ala	Phe	Asn	Ser	Pro	Tyr	Leu	Tyr	Trp	Thr	Ile	Gly	Val			
				355					360					365				
Thr	Pro	Arg	Asp	Gln	Trp	Thr	Glu	Ala	Val	Glu	Arg	Asp	Arg	Val	Ala			
				370					375					380				
Ser	Asp	Val	Pro	Ala	Asn	His	Met	Gly	Asp	Phe	Leu	Pro	Asp	Tyr	Ala			
385					390					395					400			
Pro	Thr	Met	Ser	Ala	Ala	Thr	Arg	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Thr			
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Tyr	Leu	Gly	Thr	Asn														
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<222> (101)..(3439)

<223> RXS02234

<400> 367

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	Met Pro Lys Arg Ser	
	1 5	

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc	163
Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly	
10 15 20	

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg	211
Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu	
25 30 35	

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg	259
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr	
40 45 50	

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc	307
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile	
55 60 65	

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc	355
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly	
70 75 80 85	

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt	403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu	
90 95 100	

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc	451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly	
105 110 115	

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat	499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp	
120 125 130	

cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcc	547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala	
135 140 145	

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca	595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala	
150 155 160 165	

gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc	643
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly	
170 175 180	

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct	691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala	
185 190 195	

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa	739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu	
200 205 210	

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc 787
 Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr
 215 220 225

gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg 835
 Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu
 230 235 240 245

ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg 883
 Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu
 250 255 260

act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc 931
 Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile
 265 270 275

cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc 979
 Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile
 280 285 290

aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg
 1027
 Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val
 295 300 305

tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc
 1075
 Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala
 310 315 320 325

aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc
 1123
 Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr
 330 335 340

aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac
 1171
 Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp
 345 350 355

tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc
 1219
 Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly
 360 365 370

gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg
 1267
 Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met
 375 380 385

tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc
 1315
 Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser
 390 395 400 405

ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc
 1363
 Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe
 410 415 420

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag
1411

Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys
425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt
1459

Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu
440 445 450

ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg
1507

Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp
455 460 465

ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt
1555

Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val
470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg
1603

Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met
490 495 500

ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc
1651

Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly
505 510 515

gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta
1699

Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val
520 525 530

ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg
1747

Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro
535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc
1795

Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val
550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca
1843

Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro
570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca
1891

Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala
585 590 595

gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc
1939

Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys
600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac
 1987
 Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr
 615 620 625

ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag
 2035
 Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu
 630 635 640 645

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 2083
 Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln
 650 655 660

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 2131
 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val
 665 670 675

att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag
 2179
 Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu
 680 685 690

ttc ggt gca ctg ctg aac cgc gag cag ctt cct gct cca gca ttc ggc
 2227
 Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly
 695 700 705

acc gca acc tct ttc gaa gag gct cgc aca gta gcc gat gag atc agc
 2275
 Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser
 710 715 720 725

tac cca gtg ctg gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg
 2323
 Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met
 730 735 740

gag att gtc tac gat gag gct tcc ctc gag gat tac atc aac cgc gca
 2371
 Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala
 745 750 755

act gag ttg tct tct gac cac cca gtg ctg gtt gac cgc ttc cta gac
 2419
 Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp
 760 765 770

aac gct att gag atc gac gtc gac gca ctg tgc gac ggc gac gag gtc
 2467
 Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val
 775 780 785

tac ctg gca ggc gtc atg gag cac atc gag gaa gcc ggc att cac tcc
 2515
 Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser
 790 795 800 805

ggt gac tcc gca tgt gca ctt cct cca atg act ttg ggc gca cag gac
2563

Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp
810 815 820

atc gag aag gtc cgc gaa gca acc aag aag ctg gct ctg ggc atc ggt
2611

Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly
825 830 835

gta cag ggc ctg atg aac gtc cag tac gca ctc aag gac gac atc ctc
2659

Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu
840 845 850

tac gtc atc gag gca aac cca cgt gca tcc cgc acc gtg ccg ttc gtc
2707

Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val
855 860 865

tcc aag gca acg ggc gtc aac ctg gcc aag gca gca tcc cgt atc gca
2755

Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala
870 875 880 885

gtg ggc gcc acc atc aag gat ctc caa gat gag ggc atg att cct acc
2803

Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr
890 895 900

gag tac gac ggc ggc tcc ttg cca ctg gac gct cca atc gct gtg aag
2851

Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys
905 910 915

gaa gca gtg ttg ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc
2899

Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr
920 925 930

ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg
2947

Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met
935 940 945

ggc ttg gcc aac aac ttc ggc gct gca tat gca aag gct gaa gct ggc
2995

Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly
950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct
3043

Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala
970 975 980

aac cgc gac aag cgc acc ctg atc ctg cca atc cag cgc ctg gcg ttg
3091

Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu
985 990 995

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc
3139

Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg
1000 1005 1010

cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc
3187

Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg
1015 1020 1025

gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa
3235

Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu
1030 1035 1040 1045

gtt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac
3283

Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His
1050 1055 1060

gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg
3331

Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu
1065 1070 1075

atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc
3379

Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala
1080 1085 1090

ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac
3427

Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His
1095 1100 1105

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3462

Ala Val Lys Ala
1110

<210> 368

<211> 1113

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

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20 25 30

Ala Cys Arg Val Leu Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn
35 40 45

Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr
50 55 60

Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys
65 70 75 80

Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly
 85 90 95
 Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile
 100 105 110
 Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile
 115 120 125
 Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile
 130 135 140
 Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu Val
 145 150 155 160
 His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser
 165 170 175
 Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp
 180 185 190
 Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn
 195 200 205
 Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu
 210 215 220
 Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu
 225 230 235 240
 Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val Ala
 245 250 255
 Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln
 260 265 270
 Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn
 275 280 285
 Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu
 290 295 300

Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr
 305 310 315 320
 Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr
 325 330 335
 Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe
 340 345 350
 Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe
 355 360 365
 Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser
 370 375 380
 Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn
 385 390 395 400

Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys
 405 410 415
 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val
 420 425 430
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu
 435 440 445
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser
 450 455 460
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe
 465 470 475 480
 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg
 485 490 495
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg
 500 505 510
 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu
 515 520 525
 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe
 530 535 540
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala
 545 550 555 560
 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile
 565 570 575
 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr
 580 585 590
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr
 595 600 605
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr
 610 615 620
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu
 625 630 635 640
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val
 645 650 655
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys
 660 665 670
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala
 675 680 685
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro
 690 695 700
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val
 705 710 715 720
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu

550

Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr
 1060 1065 1070

Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val
 1075 1080 1085

Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu
 1090 1095 1100

Gln Glu Leu Asp His Ala Val Lys Ala
 1105 1110

<210> 369

<211> 3221

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(3198)

<223> FRXA02234

<400> 369

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acc tac gtg gag cca atc gag ccg gaa tac atc gac aag att ttc gct 96
 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
 20 25 30

aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt 144
 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
 35 40 45

ggc ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc 192
 Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
 50 55 60

atc ctg gaa aag tac ggc gtt gaa ctc atc ggt gca gac atc gat gcc 240
 Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
 65 70 75 80

att gag cgc ggc gaa gat cgc cag aag ttc aag gat att gtc acc acc 288
 Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
 85 90 95

atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa 336
 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
 100 105 110

gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca 384
 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro
 115 120 125

tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa 432
 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu
 130 135 140

gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca 480
 Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala
 145 150 155 160

aac gtc ttg atc gaa gaa tcc atc ctt ggt tgg aag gaa ttc gag ctc 528
 Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu
 165 170 175

gag ctc atg cgc gat acc gca gac aac gtt gtg gtt atc tgc tcc att 576
 Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile
 180 185 190

gaa aac gtc gac gca ctg ggc gtg cac acc ggc gac tct gtc acc gtg 624
 Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val
 195 200 205

gca cct gcc ctg acc ctg act gac cgt gaa ttc cag aag atg cgc gat 672
 Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp
 210 215 220

cag ggt atc gcc atc atc cgc gag gtc ggc gtg gac acc ggt gga tgt 720
 Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys
 225 230 235 240

aac atc cag ttc gcc atc aac cca gtt gat ggc cgc atc atc acc att 768
 Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile
 245 250 255

gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca 816
 Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala
 260 265 270

acg ggc ttc cca att gcc aag atg gct gcc aag ctg gct atc gga tac 864
 Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr
 275 280 285

acc ctg gat gag atc acc aac gac atc act ggt gaa acc cca gct gcg 912
 Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala
 290 295 300

ttt gag ccc acc atc gac tac gtc gtg gtc aag gcc cca cgc ttt gct 960
 Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala
 305 310 315 320

ttc gag aag ttt gtc ggc gct gat gac act ttg acc acc acc atg aag
 1008
 Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys
 325 330 335

tcc gtc ggt gag gtc atg tcc ctg ggc cgc aac tac att gca gca ctg
 1056
 Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu
 340 345 350

aac aag gca ctg cgt tcc ctg gaa acc aag cag cag ggt ttc tgg acc
 1104
 Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr
 355 360 365

aag cct gat gag ttc ttc gca ggg gag cgc gct acc gat aag gca gct
 1152

Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
 370 375 380
 gtt ctg gaa gat ctc aag cgc cca acc gaa ggc cgc ctc tac gac gtt
 1200
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
 gag ctg gca atg cgc ctt ggc gca agc gtg gaa gaa ctc tac gaa gca
 1248
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
 405 410 415
 tct tct att gat cct tgg ttc ctc gcc gag ctt gaa gct ctc gtg cag
 1296
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
 420 425 430
 ttc cgc cag aag ctc gtt gac gca cca ttc cta aac gaa gat ctc ctg
 1344
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
 435 440 445
 cgc gaa gca aag ttc atg ggt ctg tcc gac ctg cag atc gca gcc ctt
 1392
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
 450 455 460
 cgc cca gag ttc gct ggc gaa gac ggc gta cgc acc ttg cgt ctg tcc
 1440
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480
 cta ggc atc cgc cca gta ttc aag act gtg gat acc tgt gca gca gag
 1488
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
 485 490 495
 ttt gaa gct aag act ccg tac cac tac tcc gca tac gag ctg gat cca
 1536
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
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 gca gct gag tct gag gtc gca cca cag act gag cgt gaa aag gtc ctg
 1584
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 atc ttg ggc tcc ggt cca aac cgc atc ggc cag ggc atc gag ttc gac
 1632
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 tac tcc tgt gtt cac gca gct ctt gag ctc tcc cgc gtc ggc tac gaa
 1680
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 act gtc atg gtc aac tgc aac cca gag acc gtg tcc acc gac tac gac
 1728
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp

565	570	575
acc gct gac cgc ctg tac ttc gag cca ctg acc ttc gaa gac gtc atg 1776		
Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met 580	585	590
gag gtc tac cac gct gag gcg cag tcc ggc acc gtc gca ggt gtt atc 1824		
Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile 595	600	605
gtc cag ctt ggt ggc cag act cct ctg ggc ttg gca gat cgt ttg aag 1872		
Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys 610	615	620
aag gct ggc gtc cct gtc att ggt acc tcc cca gag gca atc gac atg 1920		
Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met 625	630	635 640
gct gag gac cgt ggc gag ttc ggt gca ctg ctg aac cgc gag cag ctt 1968		
Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu 645	650	655
cct gct cca gca ttc ggc acc gca acc tct ttc gaa gag gct cgc aca 2016		
Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr 660	665	670
gta gcc gat gag atc agc tac cca gtg ctg gtt cgc cct tcc tac gtc 2064		
Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val 675	680	685
ttg ggt ggc cgt ggc atg gag att gtc tac gat gag gct tcc ctc gag 2112		
Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu 690	695	700
gat tac atc aac cgc gca act gag ttg tct tct gac cac cca gtg ctg 2160		
Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu 705	710	715 720
gtt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg 2208		
Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu 725	730	735
tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag 2256		
Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu 740	745	750
gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg 2304		
Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met 755	760	765

act ttg ggc gca cag gac atc gag aag gtc cgc gaa gca acc aag aag
2352

Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
770 775 780

ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca
2400

Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
785 790 795 800

ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc
2448

Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
805 810 815

cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag
2496

Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
820 825 830

gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat
2544

Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
835 840 845

gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac
2592

Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
850 855 860

gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt
2640

Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
865 870 875 880

cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag
2688

Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
885 890 895

tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat
2736

Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc
2784

Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca
2832

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc
2880

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc
3218

Leu Gln Glu Leu Asp His Ala Val Lys Ala
1060 1065

gag
3221

<210> 370

<211> 1066

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 370

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20 25 30

Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
50 55 60

Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
65 70 75 80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr

85	90	95
Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu 100 105 110		
Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro 115 120 125		
Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu 130 135 140		
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala 145 150 155 160		
Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu 165 170 175		
Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile 180 185 190		
Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val 195 200 205		
Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp 210 215 220		
Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys 225 230 235 240		
Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile 245 250 255		
Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala 260 265 270		
Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr 275 280 285		
Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala 290 295 300		
Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala 305 310 315 320		
Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys 325 330 335		
Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu 340 345 350		
Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr 355 360 365		
Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala 370 375 380		
Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val 385 390 395 400		
Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala 405 410 415		

Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
420 425 430

Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
435 440 445

Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
450 455 460

Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
465 470 475 480

Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
485 490 495

Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
500 505 510

Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
515 520 525

Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
530 535 540

Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
545 550 555 560

Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
565 570 575

Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met
580 585 590

Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile
595 600 605

Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys
610 615 620

Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met
625 630 635 640

Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu
645 650 655

Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr
660 665 670

Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val
675 680 685

Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu
690 695 700

Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu
705 710 715 720

Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu
725 730 735

Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu
 740 745 750
 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met
 755 760 765
 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
 805 810 815
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
 1010 1015 1020
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
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 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055
 Leu Gln Glu Leu Asp His Ala Val Lys Ala

1060

1065

<210> 371
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXS02565

<400> 371
 ggaaattcga tacagtgcga tgacgcgata ttagaaagaa aaagatgcgc tttagcagca 60
 aaccctcacc ctccttcagg aacttatccg caacgcctgc gtg aat gat cta acc 115
 Val Asn Asp Leu Thr
 1 5
 cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
 Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
 10 15 20
 ttt gaa gga acc ccc aac gtt aaa atc acc aag ctg gaa ccg cat ccg 211
 Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro
 25 30 35
 ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
 Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
 40 45 50
 gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
 Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
 55 60 65
 cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
 Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
 70 75 80 85
 att tgg ggt aga ggg tcc gtc gat atg ctc ttt att acc gca acc caa 403
 Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln
 90 95 100
 gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
 Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
 105 110 115
 ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
 Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
 120 125 130
 gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
 Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu Phe Ser Trp Lys Asn
 135 140 145
 tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
 Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
 150 155 160 165
 gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643

Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly Ala Ala Gln Arg Arg
 170 175 180

att cac gtc aat ggc gat gct ggt cat ggt tcc att cct ttc gac cgt 691
 Ile His Val Asn Gly Asp Ala Gly His Gly Ser Ile Pro Phe Asp Arg
 185 190 195

gac agc gct att gtc aag atc ggt gaa gtc gcc cgc cga atc gct gcc 739
 Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala Arg Arg Ile Ala Ala
 200 205 210

gcc gat ctg aag gta gcc aag gac gat atc tgg caa ggc ttc gtc caa 787
 Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp Gln Gly Phe Val Gln
 215 220 225

gcg cac cgt ttc gac cca gaa acg gag cag gcg ctt ctt agc ggg acc 835
 Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala Leu Leu Ser Gly Thr
 230 235 240 245

tcc cct gag gcc tac gca gag ttc ggc gga ctc tcc cgc ttc gcc cac 883
 Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu Ser Arg Phe Ala His
 250 255 260

gcg gtg tct cat ctc acg atc gcc caa act gtg gtt cgt gca ggt caa 931
 Ala Val Ser His Leu Thr Ile Ala Gln Thr Val Val Arg Ala Gly Gln
 265 270 275

gcc atc aat gta ttg cca tcg cat gcg tac ttg gaa ctg gat atc cgt 979
 Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu Glu Leu Asp Ile Arg
 280 285 290

acc ctt cca ggc caa acc aat gac tat gtt gat gac acc ctg cgt gct
 1027
 Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp Asp Thr Leu Arg Ala
 295 300 305

gct ctg ggc gat ctt gcc gat gaa gta gaa atc gaa cac ctc atc tct
 1075
 Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile Glu His Leu Ile Ser
 310 315 320 325

gaa gaa gca acg gtg agc cca act gat tcc agg ttg tat aac acc ttg
 1123
 Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg Leu Tyr Asn Thr Leu
 330 335 340

gaa aaa gtt ctt ggt gat ttc ttc ccc gat gcg cct gtg gtc cca att
 1171
 Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala Pro Val Val Pro Ile
 345 350 355

att tcc tct ggt ggc tct gac ctg cgc ttt ggt cgt cga cta ggc ggt
 1219
 Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly Arg Arg Leu Gly Gly
 360 365 370

gtt ggt tat ggt ttt gca gtt cat gca cgt gaa cga act ttg gcg gaa
 1267
 Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu Arg Thr Leu Ala Glu
 375 380 385

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat
1315

Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp
390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta
1363

Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu
410 415 420

ggc taaaaacatg aagcaggagt ctt

1389

Gly

<210> 372

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 372

Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu
1 5 10 15

Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys
20 25 30

Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly
35 40 45

Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val
50 55 60

Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu
65 70 75 80

Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe
85 90 95

Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly
100 105 110

Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala
115 120 125

Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu
130 135 140

Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro
145 150 155 160

Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly
165 170 175

Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser
180 185 190

Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala
195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp
 210 215 220
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala
 225 230 235 240
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu
 245 250 255
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val
 260 265 270
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu
 275 280 285
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp
 290 295 300
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile
 305 310 315 320
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg
 325 330 335
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala
 340 345 350
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly
 355 360 365
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu
 370 375 380
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala
 385 390 395 400
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val
 405 410 415
 Val Arg Glu Phe Leu Gly
 420

<210> 373
 <211> 525
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(502)
 <223> RXS02937

<400> 373
 gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60

tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115
 Val Ile Ser Asn Gly
 1 5

gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met
 10 15 20
 gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val
 25 30 35
 gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His
 40 45 50
 gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser
 55 60 65
 cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala
 70 75 80 85
 gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala
 90 95 100
 ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu
 105 110 115
 gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val
 120 125 130
 aaa taattggcta atgaatcctt ttc 525
 Lys

<210> 374

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asn Ile
 1 5 10 15
 Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr
 20 25 30
 Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala
 35 40 45
 His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val
 50 55 60
 Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala
 65 70 75 80
 Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala
 85 90 95
 Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp

100 105 110

Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala
 115 120 125

Ser Ala Trp Leu Val Lys
 130

<210> 375
 <211> 966
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(943)
 <223> RXA02194

<400> 375
 gaaatctccc agctcattta ttggacccag gtcacatgg ttgctcgagg cctgaagcca 60
 gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115
 Met Leu Lys Ile Ala
 1 5
 gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163
 Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala
 10 15 20
 gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211
 Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe
 25 30 35
 gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259
 Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile
 40 45 50
 gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307
 Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg
 55 60 65
 gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355
 Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu
 70 75 80 85
 ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403
 Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu
 90 95 100
 tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451
 Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro
 105 110 115
 aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499
 Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val
 120 125 130
 ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547
 Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala
 135 140 145

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595
 Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln
 150 155 160 165
 ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643
 Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile
 170 175 180
 gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691
 Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu
 185 190 195
 cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739
 Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp
 200 205 210
 tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787
 Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro
 215 220 225
 ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835
 Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val
 230 235 240 245
 gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883
 Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp
 250 255 260
 aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931
 Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg
 265 270 275
 atc gcc cgc atc tagttttaac taccctcgaa aat 966
 Ile Ala Arg Ile
 280

<210> 376

<211> 281

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala
 1 5 10 15
 Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys
 20 25 30
 Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu
 35 40 45
 Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu
 50 55 60
 Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His
 65 70 75 80
 Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala
 85 90 95

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile
 100 105 110

Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly
 115 120 125

Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile
 130 135 140

Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg
 145 150 155 160

Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr
 165 170 175

Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu
 180 185 190

Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn
 195 200 205

Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala
 210 215 220

Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala
 225 230 235 240

Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala
 245 250 255

Asn Ala Ile Met Asp Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu
 260 265 270

Ala Ser Glu Ile Arg Ile Ala Arg Ile
 275 280

<210> 377

<211> 393

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(370)

<223> RXA02195

<400> 377

tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccc aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag 115
 Met Tyr Arg Val Lys
 1 5

aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg
 10 15 20

cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

```

                25                30                35
cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc 259
Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala
      40                45                50

gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att 307
Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile
      55                60                65

tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat 355
Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp
      70                75                80

atc tac aag aac ctg taggagtttt aaagcaatca tgt 393
Ile Tyr Lys Asn Leu
      90

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<210> 378
 <211> 90
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 378
Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn
  1                5                10                15

Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp
      20                25                30

Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu
      35                40                45

Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu
      50                55                60

Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly
      65                70                75                80

Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu
      85                90

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<210> 379
 <211> 477
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(454)
 <223> RXA01097

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<400> 379
gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag 60

taaaggggagc cattaaagat gcaggatttg aggtgcgga atg agt gac aat cca 115
      Met Ser Asp Asn Pro
                1                5

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caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn
 10 15 20

gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu
 25 30 35

gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu
 40 45 50

gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp
 55 60 65

atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala
 70 75 80 85

ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly
 90 95 100

ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu
 105 110 115

ctg taaaagcaac aacgattaag gaa 477
 Leu

<210> 380

<211> 118

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys
 1 5 10 15

Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala
 20 25 30

Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala
 35 40 45

Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser
 50 55 60

Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu
 65 70 75 80

Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr
 85 90 95

Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe
 100 105 110

Asp Asn Asp Val Leu Leu

115

<210> 381
 <211> 861
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(838)
 <223> RXA01100

<400> 381
 gctgtgggct actcaattcc acccagaaaa atcaggtgac gcaggcgcac agctactgcg 60
 aaactggatc aactacatct aacagatagg atcaatatcc atg acc ttc act att 115
 Met Thr Phe Thr Ile
 1 5
 ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag 163
 Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln
 10 15 20
 ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca 211
 Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala
 25 30 35
 ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg 259
 Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu
 40 45 50
 gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att 307
 Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile
 55 60 65
 gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat 355
 Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp
 70 75 80 85
 gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac 403
 Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn
 90 95 100
 att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att 451
 Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile
 105 110 115
 caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa 499
 Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu
 120 125 130
 gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc 547
 Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly
 135 140 145
 gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt 595
 Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg
 150 155 160 165
 ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat 643

Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn
 170 175 180
 gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val
 185 190 195
 gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys
 200 205 210
 tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr
 215 220 225
 gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu
 230 235 240 245
 ggt taatacatgg atgctcgtgg gat 861
 Gly

<210> 382

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala
 1 5 10 15
 Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr
 20 25 30
 Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu
 35 40 45
 His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu
 50 55 60
 Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr
 65 70 75 80
 Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly
 85 90 95
 Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp
 100 105 110
 Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile
 115 120 125
 Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp
 130 135 140
 Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser
 145 150 155 160
 Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

165										170										175										
Leu	Ser	Gly	Pro	Asn	Val	Glu	Leu	Leu	Arg	Glu	Val	Ala	Ala	Ala	Thr															
			180						185					190																
Asp	Ala	Pro	Ile	Val	Ala	Ser	Gly	Gly	Ile	Ser	Val	Leu	Glu	Asp	Val															
		195					200					205																		
Leu	Glu	Leu	Ala	Lys	Tyr	Gln	Asp	Glu	Gly	Ile	Asp	Ser	Val	Ile	Ile															
	210					215					220																			
Gly	Lys	Ala	Leu	Tyr	Glu	His	Lys	Phe	Thr	Leu	Glu	Glu	Ala	Leu	Ala															
225					230					235					240															
Ala	Val	Glu	Lys	Leu	Gly																									
				245																										
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<211> 756																														
<212> DNA																														
<213> Corynebacterium glutamicum																														
<220>																														
<221> CDS																														
<222> (101)..(733)																														
<223> RXA01101																														
<400> 383																														
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cggttcttga tcttgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115																														
Met Thr Lys Thr Val 1 5																														
gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163																														
Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala 10 15 20																														
cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211																														
Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val 25 30 35																														
tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259																														
Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp 40 45 50																														
gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307																														
Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly 55 60 65																														
cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355																														
Gln Arg Leu Ala Gly Arg Pro Val Met Gly Ile Cys Val Gly Met 70 75 80 85																														
cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403																														
Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly 90 95 100																														
tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451																														
Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu																														

105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg			499
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met			
120	125	130	
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat			547
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr			
135	140	145	
ggg gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca			595
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro			
150	155	160	165
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg			643
Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val			
170	175	180	
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt			691
Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly			
185	190	195	
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc			733
Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile			
200	205	210	
taacagatag gatcaatatt cat			756

<210> 384

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg	
1 5 10 15	

Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser	
20 25 30	

Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly	
35 40 45	

Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly	
50 55 60	

His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly	
65 70 75 80	

Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly	
85 90 95	

Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu	
100 105 110	

Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro	
115 120 125	

Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr	
130 135 140	

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp
145 150 155 160

Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg
165 170 175

Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His
180 185 190

Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile
195 200 205

Asn Tyr Ile
210

<210> 385

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXN01657

<400> 385

cctccgcatc tgccgacgta tcccgcgcc tgggtgaagc catgggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcgggctg gtg atc gtt gga gtt 115
Val Ile Val Gly Val
1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
 120 125 130
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165
 caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp
 170 175 180
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu
 185 190 195
 ctg gcg att tgatgttttc ggtagcgctc tgt 723
 Leu Ala Ile
 200

<210> 386
 <211> 200
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 386
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
 1 5 10 15
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro
165 170 175

Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val
180 185 190

Arg Lys His Ala Glu Leu Ala Ile
195 200

<210> 387

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

cctccggtcat tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggtcg gtg atc gtt gga gtt 115
Val Ile Val Gly Val
1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165

caa ggc 601
 Gln Gly

<210> 388
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 388
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
 1 5 10 15

Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val Val Gly Val Arg Gln Gly
 165

<210> 389
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXA01098

<400> 389

aaaagggctc acgatgtgct gttaagtaag attgaaaaag ttcggttgat gcatgcagat 60

gcaggtaatg accagtcgtt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
 Met Gly Val Ala Ile
 1 5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
 Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
 10 15 20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
 Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
 25 30 35

aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
 Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
 40 45 50

acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
 Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
 55 60 65

acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
 Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
 70 75 80 85

agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
 Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
 90 95 100

tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
 Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
 105 110 115

tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
 Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
 120 125 130

cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
 Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
 135 140 145

acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
 Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
 150 155 160 165

aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
 Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
 170 175 180

gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
 Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
 185 190 195

gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
 Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
 200 205 210

aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val
 215 220 225

ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835
 Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val
 230 235 240 245

aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys
 250 255

tccacaagag tat 897

<210> 390
 <211> 258
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 390
 Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly
 1 5 10 15

Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp
 20 25 30

Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu
 35 40 45

Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu
 50 55 60

Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val
 65 70 75 80

Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala
 85 90 95

Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu
 100 105 110

Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu
 115 120 125

Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser
 130 135 140

Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp
 145 150 155 160

Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile
 165 170 175

Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu
 180 185 190

Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala
 195 200 205

Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val
225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val
245 250 255

Arg Lys

<210> 391

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

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gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
Met Thr Val Ala Pro
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
120 125 130

ggg gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
 135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
 150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
 200

<210> 392

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu
 1 5 10 15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
195 200

<210> 393

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA01104

<400> 393

cacttgcgca ctaccattgg tgtgcctgag gaaaatgatg cgtttttgga cgcagctgca 60

gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
Met Thr Val Ala Pro
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc caa ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
120 125 130

ggg gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
 200

<210> 394
 <211> 202
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 394
 Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu
 1 5 10 15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
 195 200

<210> 395

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<220>
<221> CDS
<222> (101)..(964)
<223> RXN00446
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584

Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285

tgc 987

<210> 396

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val
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Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

130	135	140
Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys 145	150	155 160
Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala 165	170	175
Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn 180	185	190
Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu 195	200	205
Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val 210	215	220
Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro 225	230	235 240
Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile 245	250	255
Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala 260	265	270
Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly 275	280	285

<210> 397

<211> 545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(522)

<223> FRXA00446

<400> 397

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Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr	
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ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc	96
Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile	
20 25 30	

cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat	144
His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr	
35 40 45	

ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc	192
Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile	
50 55 60	

atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca	240
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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
65 70 75 80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
85 90 95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
100 105 110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
165 170

tagtctttgg cgttttgagg tgc 545

<210> 398

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
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Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
165 170

<210> 399
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA01105

<400> 399
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gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
Met Thr Lys Ile Thr
1 5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
10 15 20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
25 30 35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
40 45 50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
55 60 65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc gcc gta 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
70 75 80 85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
90 95 100

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
105 110 115

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
120 125 130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
135 140 145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595
 Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val
 150 155 160 165

ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643
 Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp
 170 175 180

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
 Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
 185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739
 Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu
 200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787
 Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala
 215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835
 Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala
 230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883
 Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala
 250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931
 Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr
 265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979
 Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala
 280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt
 1027
 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe
 295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt
 1075
 Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe
 310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg
 1123
 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu
 330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca
 1171
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala
 345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca
 1218
 Ala Ala Glu Ile Ile Lys Leu Asn Leu
 360 365

tga
1221

<210> 400
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 400

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
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Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
20 25 30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
35 40 45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
50 55 60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
65 70 75 80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
85 90 95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
100 105 110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
115 120 125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
130 135 140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
145 150 155 160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
165 170 175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
180 185 190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
195 200 205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
210 215 220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
225 230 235 240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
245 250 255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
260 265 270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
 275 280 285
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
 290 295 300
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
 305 310 315 320
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
 325 330 335
 Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
 340 345 350
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
 355 360 365

<210> 401
 <211> 1449
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1426)
 <223> RXA01106

<400> 401
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aagaatttcg attcaacctt ttaagggaga acttttcgcc atg ttg aat gtc act 115
 Met Leu Asn Val Thr
 1 5

gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu
 10 15 20

cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211
 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro
 25 30 35

gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259
 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr
 40 45 50

ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307
 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala
 55 60 65

gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355
 Glu Val Ile Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu
 70 75 80 85

tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln
 90 95 100

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act	451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr	
105 110 115	
 gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc	499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly	
120 125 130	
 aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa	547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln	
135 140 145	
 gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag	595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu	
150 155 160 165	
 cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg	643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu	
170 175 180	
 ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
 ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
 act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
 gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
 ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
 agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
 tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
 tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	1027
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
 cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	1075
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
 gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	1123
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	

330 335 340
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc
 1171
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly
 345 350 355
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac
 1219
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His
 360 365 370
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg
 1267
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr
 375 380 385
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct
 1315
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala
 390 395 400 405
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat
 1363
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp
 410 415 420
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc
 1411
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro
 425 430 435
 acc acc gac gag gcc taagaaaaat gacccaaaatt act
 1449
 Thr Thr Asp Glu Ala
 440
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 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 402
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 1 5 10 15
 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu
 20 25 30
 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu
 35 40 45
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser
 50 55 60
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp
 65 70 75 80
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys
 85 90 95

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro
 100 105 110
 Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu
 115 120 125
 Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn
 130 135 140
 Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser
 145 150 155 160
 Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala
 165 170 175
 Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly
 180 185 190
 Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu
 195 200 205
 Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala
 210 215 220
 Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro
 225 230 235 240
 Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val
 245 250 255
 Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser
 260 265 270
 Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu
 275 280 285
 Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu
 290 295 300
 Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser
 305 310 315 320
 Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile
 325 330 335
 His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly
 340 345 350
 Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser
 355 360 365
 Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser
 370 375 380
 Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu
 385 390 395 400
 Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe
 405 410 415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala
 435 440

<210> 403

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXC00930

<400> 403

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 Met Ser Gly His Ser
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg
 25 30 35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile
 40 45 50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala
 55 60 65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn
 70 75 80 85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu
 90 95 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala
 105 110 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr
 120 125 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser
 135 140 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val
 150 155 160 165
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile
 170 175 180
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp
 185 190 195
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp
 200 205 210
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp
 215 220 225
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu
 230 235 240 245
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876
 Thr Glu Leu Glu Asn Asp
 250

<210> 404

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

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 35 40 45
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
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 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
 65 70 75 80
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
 85 90 95
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
 100 105 110
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
 115 120 125
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
 145 150 155 160
 Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
 165 170 175
 Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
 180 185 190
 Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
 195 200 205
 Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
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 Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
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 Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
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<210> 405
 <211> 547
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(547)
 <223> RXC01096

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 Met Lys Pro Arg Val
 1 5
 ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
 10 15 20
 tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
 25 30 35
 agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
 40 45 50
 gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307
 Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu
 55 60 65
 aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
 70 75 80 85
 gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

	90	95	100	
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Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys				
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gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc				499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr				
	120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta				547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu				
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<210> 406

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 406

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Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp
35 40 45

Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala
50 55 60

Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile
65 70 75 80

Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu
85 90 95

Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly
100 105 110

Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala
115 120 125

Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met
130 135 140

Ile Gly Cys Ala Leu
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<210> 407

<211> 1020

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(997)

<223> RXC01656

<400> 407

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Met Thr Glu Thr Gln
1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
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ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355
Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403
Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
90 95 100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
105 110 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787

Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val
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 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys
 230 235 240 245
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr
 250 255 260
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly
 265 270 275
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg
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 Leu Ala Glu Arg Gly Trp
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<210> 408

<211> 299

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 408

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 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
 35 40 45
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
 50 55 60
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65 70 75 80
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
 85 90 95
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
 100 105 110
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
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 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
 145 150 155 160

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										atg	tcc	att	gtt	gag		
										Met	Ser	Ile	Val	Glu		
										1				5		
cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc															163	
His	Ile	Lys	Glu	Phe	Arg	Arg	Arg	Leu	Leu	Ile	Ala	Leu	Ala	Gly	Ile	
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ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg															211	
Leu	Val	Gly	Thr	Ile	Ile	Leu	Phe	Ile	Trp	Tyr	Asp	Phe	Ser	Phe	Trp	
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cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg															259	
Gln	Ile	Pro	Thr	Leu	Gly	Glu	Leu	Leu	Arg	Asp	Pro	Tyr	Cys	Ser	Leu	
			40				45					50				
cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg															307	
Pro	Ala	Glu	Ser	Arg	Trp	Ala	Met	Ser	Asp	Ser	Glu	Glu	Cys	Arg	Leu	
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Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala	
70 75 80 85	
gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
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Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150 155 160 165	
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Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
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Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
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 Phe Gly Asp Val Leu
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<210> 410
 <211> 314
 <212> PRT
 <213> Corynebacterium glutamicum

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 Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
 35 40 45
 Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
 50 55 60
 Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65 70 75 80
 Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
 85 90 95
 Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
 100 105 110
 Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
 115 120 125
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
 130 135 140
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
 145 150 155 160
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
 165 170 175
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
 180 185 190
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
 195 200 205
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
 210 215 220
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
 225 230 235 240
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
 245 250 255
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

260 265 270
 Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu
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 Pro Gly Arg Ala Asp Phe Gly Asp Val Leu
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1390)
 <223> RXA02458

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 Met Val Phe Val Ser
 1 5
 gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly
 10 15 20
 ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac 211
 Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn
 25 30 35
 cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att 259
 Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile
 40 45 50
 gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc 307
 Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg
 55 60 65
 agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt 355
 Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val
 70 75 80 85
 gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt 403
 Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly
 90 95 100
 acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct 451
 Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro
 105 110 115
 gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc 499
 Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser
 120 125 130

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 Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn
 135 140 145

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 Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val
 150 155 160 165

gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt 643
 Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu
 170 175 180

tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt 691
 Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly
 185 190 195

cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt 739
 Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg
 200 205 210

tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat 787
 Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His
 215 220 225

cct ggt gag atc ttg ggt ccg acc tgg cgc att gag ccg gat ctt tct 835
 Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser
 230 235 240 245

aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc 883
 Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile
 250 255 260

aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att 931
 Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile
 265 270 275

cgt tgc att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag 979
 Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln
 280 285 290

ggt gaa ggt tac gat ctg tgc gtg act ggt ccg gtt gct ctc aag ggc
 1027
 Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly
 295 300 305

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 1075
 Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala
 310 315 320 325

gcg ttg gct gcg ttg gcg tgc aca gag tct cgt ttg acc ggt att gct
 1123
 Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala
 330 335 340

cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag
 1171
 His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu
 345 350 355

atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg
1219

Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu
360 365 370

att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat
1267

Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp
375 380 385

cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc
1315

His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly
390 395 400 405

gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt
1363

Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe
410 415 420

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Glu Asn Val Trp Glu Glu Met Val Gly
425 430

ccg
1413

<210> 412

<211> 430

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

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20 25 30

Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr
35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met
50 55 60

Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val
65 70 75 80

Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu
85 90 95

Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala
100 105 110

Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val
115 120 125

Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu
130 135 140

Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro
 145 150 155 160
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val
 165 170 175
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val
 180 185 190
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr
 195 200 205
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn
 210 215 220
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile
 225 230 235 240
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Val
 245 250 255
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln
 260 265 270
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val
 275 280 285
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro
 290 295 300
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu
 305 310 315 320
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg
 325 330 335
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala
 340 345 350
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu
 355 360 365
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp
 370 375 380
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly
 385 390 395 400
 Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys
 405 410 415
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 420 425 430

<210> 413

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1243)

<223> RXA02790

<400> 413

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gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
                        10                               15                               20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
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acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
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Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser
                        70                               75                               80                               85

aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln
                        90                               95                               100

gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451
Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp
                        105                               110                               115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp
                        120                               125                               130

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile
                        135                               140                               145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu
                        150                               155                               160                               165

gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc 643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val
                        170                               175                               180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys
                        185                               190                               195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739

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Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser
 200 205 210
 aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac 787
 Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn
 215 220 225
 cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt 835
 His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu
 230 235 240 245
 act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca 883
 Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala
 250 255 260
 cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc 931
 Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu
 265 270 275
 gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg 979
 Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu
 280 285 290
 tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc
 1027
 Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
 295 300 305
 cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
 1075
 Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
 310 315 320 325
 gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga
 1123
 Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
 330 335 340
 aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc
 1171
 Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
 345 350 355
 aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac
 1219
 Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
 360 365 370
 agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaat tgg
 1266
 Ser Gly Val Leu Asp Ser Asn Arg
 375 380
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 <211> 381
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 <213> Corynebacterium glutamicum
 <400> 414
 Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr

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Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val	20	25	30
Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly	35	40	45
Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu	50	55	60
Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe	65	70	75
Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly	85	90	95
Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala	100	105	110
Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly	115	120	125
Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly	130	135	140
Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn	145	150	155
Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro	165	170	175
Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg	180	185	190
Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr	195	200	205
Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile	210	215	220
Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala	225	230	235
Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu	245	250	255
Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val	260	265	270
Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr	275	280	285
Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp	290	295	300
Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro	305	310	315
Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu	325	330	335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
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Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
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Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
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<210> 415

<211> 644

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(621)

<223> RXN00954

<400> 415

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gcg tac aac cct gcg att gcg cat gtg cag ccg gtt cgc cag gcg ctg 96
 Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
 20 25 30

aaa ttc ccc acc atc ttc aac acg ctt gga cca ttg ctg tcc ccg gcg 144
 Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
 35 40 45

cgc ccg gag cgt cag atc atg gcc gtg gcc aat gcc aat cat gga cag 192
 Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
 50 55 60

ctc atc gcc gag gtc ttc cgc gag ttg gcc cgt aca cgc gcg ctt gtt 240
 Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
 65 70 75 80

gtg cat gcc gca gcc acc gat gag atc gca gtc cac gcc acc acc ttg 288
 Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
 85 90 95

gtg tgg gag ctt aaa gaa gac gcc acc atc gag cat tac acc atc gag 336
 Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
 100 105 110

cct gag gac ctt gcc ctt gcc cgc tac acc ctt gag gat ctc gta ggt 384
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
 115 120 125

ggc ctc gcc act gag aac gcc gaa gct atg cgc gct act ttc gcg gcc 432
 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
 130 135 140

acc gcc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480
 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
 145 150 155 160

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
 165 170 175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
 180 185 190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621
 Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp
 195 200 205

tagtaataat ctgcccacag tgt 644

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 <211> 207
 <212> PRT
 <213> Corynebacterium glutamicum

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Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
 20 25 30

Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
 35 40 45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
 50 55 60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
 65 70 75 80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
 85 90 95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
 100 105 110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
 115 120 125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
 130 135 140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
 145 150 155 160

Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
 165 170 175

Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
 180 185 190

Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp
 195 200 205

<210> 417

<211> 611

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(588)

<223> FRXA00954

<400> 417

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   1             5             10             15

gtt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca      96
Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro
           20             25             30

ttg ctg tcc ccg gcg cgc ccg gag cgt cag atc atg ggc gtg gcc aat     144
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
       35             40             45

gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt     192
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
       50             55             60

aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc     240
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
       65             70             75             80

cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag     288
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
           85             90             95

cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt     336
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
           100            105            110

gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc     384
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
           115            120            125

gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct     432
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
           130            135            140

gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg     480
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
           145            150            155            160

aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc     528
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
           165            170            175

cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag     576
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
           180            185            190

tct tcc aat gac tagtaataat ctgcccacag tgt                             611

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Ser Ser Asn Asp
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<212> PRT
<213> Corynebacterium glutamicum

<400> 418
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Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
35 40 45
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
50 55 60
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
65 70 75 80
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
85 90 95
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
100 105 110
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
115 120 125
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
130 135 140
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
145 150 155 160
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
165 170 175

Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
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Ser Ser Asn Asp
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<210> 419
<211> 1677
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1654)
<223> RXN00957

<400> 419

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aaggcttcag ccccaaatg atttctcgg taggtgcccc atg agc acg aat ccc 115
Met Ser Thr Asn Pro
1 5
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu
10 15 20
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu
25 30 35
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu
40 45 50
aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln
55 60 65
ccg ctg acg gac tcg ggt agg gca gtg gtt gcg cgc cta acg cag cag 355
Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln
70 75 80 85
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser
90 95 100
gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu
105 110 115
gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu
120 125 130
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu
135 140 145
acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln
150 155 160 165
ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr
170 175 180
gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu
185 190 195
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu
200 205 210
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val
215 220 225

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa 835
 Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys
 230 235 240 245

gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act 883
 Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr
 250 255 260

ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt 931
 Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg
 265 270 275

gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa 979
 Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu
 280 285 290

ggc cgc tcc tat gaa ctt ttt ggc gca tcc cct gag tcc aac ctc aag
 1027
 Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys
 295 300 305

ttc acc gct gct aac cgt gag ctg cag ctg tac cca atc gca ggt acc
 1075
 Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr
 310 315 320 325

cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat
 1123
 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp
 330 335 340

atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag
 1171
 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu
 345 350 355

cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg
 1219
 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser
 360 365 370

~~gtc cca ggc tcg cgc cgg gtt ggc gat ctt ttg cag gtg gat cgc tat~~
 1267
 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr
 375 380 385

tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca
 1315
 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro
 390 395 400 405

gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg
 1363
 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr
 410 415 420

ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc
 1411
 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val
 425 430 435

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc
1459

Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg
440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tgc gcg ttt gtc
1507

Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val
455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat
1555

Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp
470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc
1603

Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala
490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc
1651

Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile
505 510 515

cga tgacacacgt tgttctcatt gat
1677

Arg

<210> 420

<211> 518

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser
35 40 45

Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn
50 55 60

Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala
65 70 75 80

Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe
85 90 95

Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala
100 105 110

Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr
115 120 125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe
 130 135 140
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr
 145 150 155 160
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn
 165 170 175
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly
 180 185 190
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala
 195 200 205
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp
 210 215 220
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln
 225 230 235 240
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val
 245 250 255
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala
 260 265 270
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile
 275 280 285
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro
 290 295 300
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr
 305 310 315 320
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile
 325 330 335
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala
 340 345 350

Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp
 355 360 365
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu
 370 375 380
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr
 385 390 395 400
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys
 405 410 415
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu
 420 425 430
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala
 435 440 445

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu
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Thr Leu Glu Val Ile Arg
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<210> 421

<211> 1151

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1128)

<223> FRXA00957

<400> 421

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aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac	96
Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp	
20 25 30	
atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc	144
Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala	
35 40 45	
cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac	192
Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp	
50 55 60	
gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac	240
Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp	
65 70 75 80	
ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc	288
Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg	
85 90 95	
acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac	336
Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr	
100 105 110	
caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc	384
Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe	
115 120 125	
gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc	432
Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe	

130	135	140	
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Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser	Tyr Glu Leu Phe Gly Ala		
145	150 155 160		
tcc cct gag tcc aac ctc aag ttc acc gct gct	aac cgt gag ctg cag	528	
Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala	Asn Arg Glu Leu Gln		
165	170 175		
ctg tac cca atc gca ggt acc cgc ccc cgt gga	ctc aac cca gat ggc	576	
Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg	Gly Leu Asn Pro Asp Gly		
180	185 190		
tcc atc aac gat gag cta gat atc cgc aat gag	ttg gat atg cgc act	624	
Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn	Glu Leu Asp Met Arg Thr		
195	200 205		
gat gcc aaa gag atc gcg gag cac acc atg ctt	gtc gat ctc gcc cgc	672	
Asp Ala Lys Glu Ile Ala Glu His Thr Met	Leu Val Asp Leu Ala Arg		
210	215 220		
aac gac ctg gcc cgc gtc tcg gtc cca gcg	tcg cgc cgg gtt gcg gat	720	
Asn Asp Leu Ala Arg Val Ser Val Pro Ala	Ser Arg Arg Val Ala Asp		
225	230 235 240		
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg	cac ttg gtg tcc cgt	768	
Leu Leu Gln Val Asp Arg Tyr Ser Arg Val	Met His Leu Val Ser Arg		
245	250 255		
gtg acg gcg acg ttg gac cca gag ctt gat gct	ttg gac gcc tat cgg	816	
Val Thr Ala Thr Leu Asp Pro Glu Leu Asp	Ala Leu Asp Ala Tyr Arg		
260	265 270		
gcg tgc atg aat atg ggc acg ttg acc ggc gct	ccg aag ttg cgc gct	864	
Ala Cys Met Asn Met Gly Thr Leu Thr Gly	Ala Pro Lys Leu Arg Ala		
275	280 285		
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg	cgt ggt tct tat ggt	912	
Met Glu Leu Leu Arg Gly Val Glu Lys Arg	Arg Arg Gly Ser Tyr Gly		
290	295 300		
ggg gca gta gga tac ctg cgc ggc aat ggc	gat atg gat aat tgc att	960	
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly	Asp Met Asp Asn Cys Ile		
305	310 315 320		
gtt att cgt tcg gcg ttt gtc cag gat ggt	gtg gct gct gtg cag gct	1008	
Val Ile Arg Ser Ala Phe Val Gln Asp Gly	Val Ala Ala Val Gln Ala		
325	330 335		
ggt gct ggt gtg gtc cgc gat tct aat cct	caa tct gaa gcc gat gag	1056	
Gly Ala Gly Val Val Arg Asp Ser Asn Pro	Gln Ser Glu Ala Asp Glu		
340	345 350		
acg ttg cac aag gcg tat gcc gtg ttg aat	gcc att gcg ctt gct gct	1104	
Thr Leu His Lys Ala Tyr Ala Val Leu Asn	Ala Ile Ala Leu Ala Ala		
355	360 365		

ggt tcc act ttg gag gtc atc cga tgacacacgt tgttctcatt gat

1151

Gly Ser Thr Leu Glu Val Ile Arg
370 375

<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

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Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp
20 25 30

Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
35 40 45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
50 55 60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
65 70 75 80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
85 90 95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
100 105 110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
115 120 125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe
130 135 140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala
145 150 155 160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln
165 170 175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly
180 185 190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr
195 200 205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg
210 215 220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp
225 230 235 240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg
245 250 255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg

260	265	270
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala		
275	280	285
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly		
290	295	300
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile		
305	310	315
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala		
325	330	335
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu		
340	345	350
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala		
355	360	365
Gly Ser Thr Leu Glu Val Ile Arg		
370	375	

<210> 423

<211> 1068

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> RXA02687

<400> 423

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Met Ser Asp Ala Pro	
1 5	

act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc	163
Thr Val Val Ala Thr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala	
10 15 20	

ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag	211
Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu	
25 30 35	

cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac	259
Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His	
40 45 50	

ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc	307
Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly	
55 60 65	

ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa	355
Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln	
70 75 80 85	

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val
 105 110 115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala
 120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala
 135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595
 Glu Gly Thr Ala Asp Ala Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu
 150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala
 170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro
 185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro
 200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp
 215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr
 230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala
 250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val
 265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp
 280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc
 1027
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser
 295 300 305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att
 1068
 Glu Gly Arg Lys Leu Asn
 310 315

<210> 424
 <211> 315
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 424

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Met Ser Asp Ala Pro Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr
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Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly
              20              25              30

Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val
              35              40              45

Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu
              50              55              60

Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln
              65              70              75              80

Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe
              85              90              95

Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu
              100              105              110

Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr
              115              120              125

Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly
              130              135              140

Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser
              145              150              155              160

Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala
              165              170              175

Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala
              180              185              190

Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser
              195              200              205

Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala
              210              215              220

Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys
              225              230              235              240

Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg
              245              250              255

Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu
              260              265              270

Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser
              275              280              285
  
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Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp
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Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn
 305 310 315

<210> 425

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> RXN01698

<400> 425

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gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115
 Met Leu Gly Met Leu
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa	595
Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu	
150 155 160 165	
acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc	643
Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser	
170 175 180	
gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc	691
Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile	
185 190 195	
gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg	739
Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met	
200 205 210	
atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc	787
Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly	
215 220 225	
atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac	835
Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His	
230 235 240 245	
att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg	883
Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met	
250 255 260	
ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa	931
Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu	
265 270 275	
gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac	979
Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp	
280 285 290	
aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc	
1027	
Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly	
295 300 305	
atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att	
1075	
Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile	
310 315 320 325	
tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag	
1123	
Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys	
330 335 340	
gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc	
1171	
Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala	
345 350 355	
gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca	
1219	
Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala	
360 365 370	

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac
1267

Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn
375 380 385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt
1315

Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly
390 395 400 405

tta gag gat gga gcg taatgaagtg aatgatcaaa ttc
1353

Leu Glu Asp Gly Ala
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<210> 426

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Met Leu Gly Met Leu Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln
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Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr
20 25 30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly
35 40 45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr
50 55 60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile
65 70 75 80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
85 90 95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
100 105 110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
115 120 125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
130 135 140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
145 150 155 160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
165 170 175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
180 185 190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
195 200 205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 210 215 220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 225 230 235 240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 245 250 255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 260 265 270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
 275 280 285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
 290 295 300

Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala
 305 310 315 320

Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 370 375 380

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 385 390 395 400

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 405 410

<210> 427

<211> 1013

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(990)

<223> FRXA01698

<400> 427

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ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly

35	40	45	
atg ctc aag tac gga ttc gat gat gcc cgc aac gtg ctg gag cgt tct			192
Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser			
50	55	60	
tca gcc cgt gag acg gca gca cgc gtg gca gca gca acc gtt gcg cgt			240
Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg			
65	70	75	80
tcc ttc ctg cgt gaa acc ttg ggc gtg gaa gtg ctt tcc cac gta att			288
Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile			
	85	90	95
tcc att ggt gcg tcc gag cct tac act ggc gcg gag cca acc ttt gca			336
Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala			
	100	105	110
gat att caa gca atc gat gat tcc cca gtt cgt gca ttc ggt aaa gac			384
Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp			
	115	120	125
gct gaa gaa tcc atg atc gcg gaa atc gag gcc gca aag aaa gcc ggc			432
Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly			
	130	135	140
gat acc ctc ggt ggc atc gtg gaa gtg att gtt gaa ggc ctg ccc atc			480
Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile			
145	150	155	160
ggt ttg ggc tca cac att tct ggc gaa gat cgc ctc gat gcg cag atc			528
Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile			
	165	170	175
gca gct gca ctc atg ggc att cag gcc atc aag ggc gtg gaa atc ggt			576
Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly			
	180	185	190
gac ggt ttc gaa gaa gct cgt cga cgt ggc tcc gaa gcc cac gat gaa			624
Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu			
	195	200	205
gtg ttc ctg gat gac aac ggc gta tac cgc aac acc aac cgt gca ggt			672
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly			
	210	215	220
ggc ctc gaa ggc ggc atg acc aac ggt gaa acc ctg cgc gtt cgt gct			720
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala			
225	230	235	240
ggc atg aag cca att tct act gtg cct cgc gcc ctg aaa acc att gat			768
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp			
	245	250	255
atg gaa aac ggc aag gca gca acc gga atc cac cag cgt tcc gac gtg			816
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val			
	260	265	270
tgc gct gtt cca gcc gcc ggt gtc gtt gca gaa gca atg gtc acc ctg			864
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu			
	275	280	285

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa
 1010
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 325 330

ttc
 1013

<210> 428

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

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Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu

195	200	205
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220		
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240		
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255		
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270		
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285		
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser 290 295 300		
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg 305 310 315 320		
Met Lys Phe Glu Gly Leu Glu Asp Gly Ala 325 330		

<210> 429
 <211> 906
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(883)
 <223> RXA01095

<400> 429
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 ataaccttaa acacagcatt ggttggaagg aggttggggc atg gtt gca aca gag 115
 Met Val Ala Thr Glu
 1 5
 aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca 163
 Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala
 10 15 20
 acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc 211
 Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu
 25 30 35
 acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat 259
 Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn
 40 45 50
 gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg 307
 Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser
 55 60 65
 gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg 355

Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met	
70 75 80 85	
ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat	403
Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp	
90 95 100	
atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat	451
Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp	
105 110 115	
ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc	499
Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile	
120 125 130	
gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa	547
Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu	
135 140 145	
tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct	595
Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser	
150 155 160 165	
gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca	643
Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr	
170 175 180	
gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct	691
Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro	
185 190 195	
gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc	739
Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg	
200 205 210	
att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca	787
Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala	
215 220 225	
cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc	835
Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr	
230 235 240 245	
aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt	883
Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg	
250 255 260	
tgaagagggtg ctctgtggtc agc	906
<210> 430	
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<212> PRT	
<213> Corynebacterium glutamicum	
<400> 430	
Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile	
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Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser	
20 25 30	

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe
 35 40 45
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn
 50 55 60
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly
 65 70 75 80
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp
 85 90 95
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro
 100 105 110
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala
 115 120 125
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu
 130 135 140
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met
 145 150 155 160
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val
 165 170 175
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly
 180 185 190
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro
 195 200 205
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu
 210 215 220
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His
 225 230 235 240
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro
 245 250 255
 Ala Cys Pro Ser Arg
 260

<210> 431
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1522)
 <223> RXA00955

<400> 431
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 aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115

											Met	Thr	Ser	Asn	Asn	
											1				5	
ctg	ccc	aca	gtg	ttg	gaa	agc	atc	gtc	gag	ggg	cgt	cgc	gga	cac	ctg	163
Leu	Pro	Thr	Val	Leu	Glu	Ser	Ile	Val	Glu	Gly	Arg	Arg	Gly	His	Leu	
			10						15					20		
gag	gaa	att	cgc	gct	cgc	atc	gct	cac	gtg	gat	gtg	gat	gcg	ctt	cca	211
Glu	Glu	Ile	Arg	Ala	Arg	Ile	Ala	His	Val	Asp	Val	Asp	Ala	Leu	Pro	
			25					30					35			
aaa	tcc	acc	cgt	tct	ctg	ttt	gat	tcc	ctc	aac	cag	ggg	agg	gga	ggg	259
Lys	Ser	Thr	Arg	Ser	Leu	Phe	Asp	Ser	Leu	Asn	Gln	Gly	Arg	Gly	Gly	
		40					45					50				
gcg	cgt	ttc	atc	atg	gag	tgc	aag	tcc	gca	tcg	cct	tct	ttg	gga	atg	307
Ala	Arg	Phe	Ile	Met	Glu	Cys	Lys	Ser	Ala	Ser	Pro	Ser	Leu	Gly	Met	
	55					60					65					
att	cgt	gag	cac	tac	cag	ccg	ggg	gaa	atc	gct	cgc	gtg	tac	tct	cgc	355
Ile	Arg	Glu	His	Tyr	Gln	Pro	Gly	Glu	Ile	Ala	Arg	Val	Tyr	Ser	Arg	
	70				75					80					85	
tac	gcc	agc	ggc	att	tcc	gtg	ctg	tgc	gag	ccg	gat	cgt	ttt	ggg	ggc	403
Tyr	Ala	Ser	Gly	Ile	Ser	Val	Leu	Cys	Glu	Pro	Asp	Arg	Phe	Gly	Gly	
			90					95						100		
gat	tac	gat	cac	ctc	gct	acc	gtt	gcc	gct	acc	tct	cat	ctt	ccg	gtg	451
Asp	Tyr	Asp	His	Leu	Ala	Thr	Val	Ala	Ala	Thr	Ser	His	Leu	Pro	Val	
			105					110					115			
ctg	tgc	aaa	gac	ttc	atc	att	gat	cct	gtc	cag	gta	cac	gcg	gcg	cgt	499
Leu	Cys	Lys	Asp	Phe	Ile	Ile	Asp	Pro	Val	Gln	Val	His	Ala	Ala	Arg	
		120					125					130				
tac	ttt	ggg	gct	gat	gcc	atc	ctg	ctc	atg	ctc	tct	gtg	ctt	gat	gat	547
Tyr	Phe	Gly	Ala	Asp	Ala	Ile	Leu	Leu	Met	Leu	Ser	Val	Leu	Asp	Asp	
	135					140					145					
gaa	gag	tac	gca	gca	ctc	gct	gcc	gag	gct	gcg	cgt	ttt	gat	ctg	gat	595
Glu	Glu	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Arg	Phe	Asp	Leu	Asp	
150					155					160				165		
atc	ctc	acc	gag	gtt	att	gat	gag	gag	gaa	gtc	gcc	cgc	gcc	atc	aag	643
Ile	Leu	Thr	Glu	Val	Ile	Asp	Glu	Glu	Glu	Val	Ala	Arg	Ala	Ile	Lys	
			170						175					180		
ctg	ggg	gcg	aag	atc	ttt	ggc	gtc	aac	cac	cgc	aac	ctg	cat	gat	ctg	691
Leu	Gly	Ala	Lys	Ile	Phe	Gly	Val	Asn	His	Arg	Asn	Leu	His	Asp	Leu	
			185					190				195				
tcc	att	gat	ttg	gat	cgt	tca	cgt	cgc	ctg	tcc	aag	ctc	att	cca	gca	739
Ser	Ile	Asp	Leu	Asp	Arg	Ser	Arg	Arg	Leu	Ser	Lys	Leu	Ile	Pro	Ala	
		200					205					210				
gat	gcc	gtg	ctc	gtg	tct	gag	tct	ggc	gtg	cgc	gat	acc	gaa	acc	gtc	787
Asp	Ala	Val	Leu	Val	Ser	Glu	Ser	Gly	Val	Arg	Asp	Thr	Glu	Thr	Val	
	215					220				225						
cgc	cag	cta	ggg	ggg	cac	tcc	aat	gca	ttc	ctc	gtt	ggc	tcc	cag	ctg	835
Arg	Gln	Leu	Gly	Gly	His	Ser	Asn	Ala	Phe	Leu	Val	Gly	Ser	Gln	Leu	

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc				883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly				
	250	255	260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct				931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala				
	265	270	275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg				979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser				
	280	285	290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027				
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu				
	295	300	305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075				
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys				
310	315	320	325	
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123				
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu				
	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171				
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu				
	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219				
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser				
	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267				
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys				
	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315				
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp				
390	395	400	405	
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363				
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly				
	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411				
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly				
	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga
 1545

Ser Thr Phe His Tyr
 470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly
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Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg
 210 215 220

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu
 225 230 235 240
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg
 245 250 255
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser
 260 265 270
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile
 275 280 285
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys
 290 295 300
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg
 305 310 315 320
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln
 325 330 335
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile
 340 345 350
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala
 355 360 365
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu
 370 375 380
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly
 385 390 395 400
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser
 405 410 415
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala
 420 425 430
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala
 435 440 445
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys
 450 455 460
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr
 465 470

<210> 433

<211> 494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(471)

<223> RXA02814

<400> 433

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gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc 48
Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1          5          10          15

atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
  65          70          75          80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
          85          90          95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
          100          105          110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
          115          120          125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
          130          135          140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
          145          150          155

tcttaaaaca ccg 494

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<210> 434

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

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Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1          5          10          15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

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His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
65 70 75 80

Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
85 90 95

Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
100 105 110

Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
115 120 125

Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
130 135 140

Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
145 150 155

<210> 435

<211> 803

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(780)

<223> RXA00229

<400> 435

gag gcg aaa ggc ctc gcg cag gga cgt gcg acg gtg tac agg cgc atc 48
Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
1 5 10 15

gac acg ctt ggg tgc cgt gct tcc ggg caa gat tta aat acg ctt ctc 96
Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
20 25 30

gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144
Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
35 40 45

tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192
Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
50 55 60

acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240
Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
65 70 75 80

acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288
Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
85 90 95

gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336
Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
100 105 110

ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384
Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140

gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160

gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175

aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190

gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205

ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220

acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240

cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255

ttc ctg tcc ctc taaaagagtc agtaaaacct cga 803
 Phe Leu Ser Leu
 260

<210> 436

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
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Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30

Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45

Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60

Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80

Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255
 Phe Leu Ser Leu
 260

<210> 437
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXA02093

<400> 437
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 Met Val Asn Tyr Val
 1 5
 gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163
 Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn
 10 15 20
 cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn
 25 30 35
 tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr	Leu	Tyr	Lys	Ala	Val	Ala	Pro	Ala	Asp	Ile	Thr	Ala	Ala	Val	Ala		
		40					45					50					
ggt	atc	cgt	ggt	ctg	aac	att	cgc	ggc	gca	ggt	gtc	tcc	atg	cca	tac	307	
Gly	Ile	Arg	Gly	Leu	Asn	Ile	Arg	Gly	Ala	Gly	Val	Ser	Met	Pro	Tyr		
		55				60					65						
aag	agc	gat	gtc	atc	cca	ctc	atc	gat	gag	ttg	cat	cct	tcc	gca	gag	355	
Lys	Ser	Asp	Val	Ile	Pro	Leu	Ile	Asp	Glu	Leu	His	Pro	Ser	Ala	Glu		
		70			75					80					85		
cgc	ata	cgt	tct	gtt	aac	acc	atc	gtc	aac	aat	gac	gga	cac	ctt	gtc	403	
Arg	Ile	Arg	Ser	Val	Asn	Thr	Ile	Val	Asn	Asn	Asp	Gly	His	Leu	Val		
				90					95					100			
gga	tac	aac	acc	gac	tac	act	gcg	gtg	tac	cac	ctc	ctt	gaa	gaa	cac	451	
Gly	Tyr	Asn	Thr	Asp	Tyr	Thr	Ala	Val	Tyr	His	Leu	Leu	Glu	Glu	His		
			105					110					115				
cgc	gtg	aac	ccc	aat	gca	cga	gta	gct	atc	aag	gga	tcc	ggc	ggc	atg	499	
Arg	Val	Asn	Pro	Asn	Ala	Arg	Val	Ala	Ile	Lys	Gly	Ser	Gly	Gly	Met		
			120				125					130					
gcc	aat	gct	gtt	gtt	gca	gct	ctt	gct	gag	tat	ggt	ctg	agt	ggc	acc	547	
Ala	Asn	Ala	Val	Val	Ala	Ala	Leu	Ala	Glu	Tyr	Gly	Leu	Ser	Gly	Thr		
			135				140					145					
gtc	gtt	gcc	cgc	aac	cac	acc	acc	ggt	tct	gcg	cta	gct	tcc	cgt	tac	595	
Val	Val	Ala	Arg	Asn	His	Thr	Thr	Gly	Ser	Ala	Leu	Ala	Ser	Arg	Tyr		
					155					160					165		
ggt	tgg	gaa	tac	tcc	gca	act	gtt	ccg	gaa	gac	gca	aaa	att	ttg	gtt	643	
Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170					175					180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct	691	
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta	739	
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
			200				205						210				

gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt	787	
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
			215				220				225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag	835	
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
			230			235				240					245		
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att	883	
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
				250					255					260			
gct	gcg	gag	gag	ttc	tcc	aag	taaatttctc	tcccctatatt	tta							927	
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
				265													

<210> 438

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 438

Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala
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Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala
 20 25 30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile
 35 40 45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly
 50 55 60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu
 65 70 75 80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn
 85 90 95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His
 100 105 110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys
 115 120 125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr
 130 135 140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala
 145 150 155 160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp
 165 170 175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp
 180 185 190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val
 195 200 205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu
 210 215 220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala
 225 230 235 240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr
 245 250 255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys
 260 265

<210> 439

<211> 951

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXA02791

<400> 439

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ggcgttctag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115
                                Leu Gly Ser His Ile
                                1 5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                10 15 20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                25 30 35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                40 45 50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                55 60 65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                70 75 80 85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                90 95 100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                105 110 115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                120 125 130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                135 140 145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                150 155 160 165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                170 175 180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                185 190 195

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gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp
 200 205 210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala
 215 220 225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser
 230 235 240 245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala
 250 255 260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His
 265 270 275

taagtccccc ccacctctc aac 951

<210> 440

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile
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Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu
 20 25 30

Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met
 35 40 45

Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser
 50 55 60

Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val
 65 70 75 80

Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr
 85 90 95

Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly
 100 105 110

Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala
 115 120 125

Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu
 130 135 140

Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg
 145 150 155 160

Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala
 165 170 175

Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser
 180 185 190
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile
 195 200 205
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val
 210 215 220
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met
 225 230 235 240
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp
 245 250 255
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile
 260 265 270
 Ser Glu Glu His
 275

<210> 441
 <211> 693
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(670)
 <223> RXA01699

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 aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115
 Met Glu Arg Asn Glu
 1 5
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu
 10 15 20

tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys
 25 30 35
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val
 40 45 50
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala
 55 60 65
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile
 70 75 80 85
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403

His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly
 90 95 100

gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451
 Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp
 105 110 115

gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499
 Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala
 120 125 130

aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547
 Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His
 135 140 145

tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595
 Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala
 150 155 160 165

acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643
 Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala
 170 175 180

gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690
 Ala Val Leu His His Leu Glu Ile Asp
 185 190

tta 693

<210> 442
 <211> 190
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 442
 Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
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Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
 20 25 30

Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
 35 40 45

Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
 50 55 60

Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
 65 70 75 80

Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
 85 90 95

Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
 100 105 110

Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
 115 120 125

Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

130 135 140

Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu
145 150 155 160

Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro
165 170 175

Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp
180 185 190

<210> 443
<211> 959
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (97)..(936)
<223> RXA00952

<400> 443
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cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat 114
Met Ser Arg Tyr Asp Asp
1 5

ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc 162
Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe
10 15 20

atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc 210
Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser
25 30 35

aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc 258
Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe
40 45 50

tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc 306
Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg
55 60 65 70

gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag 354
Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys
75 80 85

cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac 402
Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr
90 95 100

ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc 450
Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe
105 110 115

gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga 498
Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg
120 125 130

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro
 135 140 145 150

 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val
 155 160 165

 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val
 170 175 180

 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val
 185 190 195

 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly
 200 205 210

 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser
 215 220 225 230

 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys
 235 240 245

 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu
 250 255 260

 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys
 265 270 275

 aag gtt taggccttta aatgtggcaa tgt 959
 Lys Val
 280

<210> 444

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu
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 Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu
 20 25 30

 Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu
 35 40 45

 Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val
 50 55 60

 Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser
 65 70 75 80

Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro
85 90 95

Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp
100 105 110

Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu
115 120 125

Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala
130 135 140

Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu
145 150 155 160

Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala
165 170 175

Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp
180 185 190

Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro
195 200 205

Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala
210 215 220

Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys
225 230 235 240

Ile Ile Ala Ser His Cys Glu Gly Glu His Pro Asn Pro Ser Thr Ile
245 250 255

Arg Asp Met Asp Gly Leu Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala
260 265 270

Met Lys Ala Ala Thr Lys Lys Val
275 280

<210> 445

<211> 1237

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1237)

<223> RXN00956

<400> 445

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accatctcca cattccatta ctaaaggttt aaataggatc atg act gaa aaa gaa 115
Met Thr Glu Lys Glu
1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
 1219
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc gaa gta
 1237
 Ala Lys Thr Ala Glu Val
 375

<210> 446

<211> 379

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 446

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr
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Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
 20 25 30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

85	90	95
Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg 100 105 110		
Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly 115 120 125		
Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val 130 135 140		
Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg 145 150 155 160		
Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly 165 170 175		
Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr 180 185 190		
Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro 195 200 205		
Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala 210 215 220		
Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val 225 230 235 240		
Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe 245 250 255		
Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu 260 265 270		
Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile 275 280 285		
Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly 290 295 300		
Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly 305 310 315 320		
Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr 325 330 335		
Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala 340 345 350		
Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala 355 360 365		
Tyr Ala Leu Lys Arg Ala Lys Thr Ala Glu Val 370 375		

<210> 447

<211> 1231

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> FRXA00956

<400> 447

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                                         Met Thr Glu Lys Glu
                                         1                               5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
                               10                               15                               20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu
                               25                               30                               35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu
                               40                               45                               50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu
                               55                               60                               65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile
                               70                               75                               80                               85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn
                               90                               95                               100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg
                               105                               110                               115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu
                               120                               125                               130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys
                               135                               140                               145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly
                               150                               155                               160                               165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala
                               170                               175                               180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His
                               185                               190                               195

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tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg 739
 Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val
 200 205 210

cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta 787
 Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu
 215 220 225

gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt 835
 Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly
 230 235 240 245

ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt 883
 Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly
 250 255 260

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc gcc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
 1211
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc
 1231
 Ala Lys Thr Ala
 375

<210> 448

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 448

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 Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
 20 25 30
 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
 85 90 95
 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
 100 105 110
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
 115 120 125
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
 130 135 140
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
 145 150 155 160
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
 165 170 175
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
 180 185 190
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
 195 200 205
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
 210 215 220
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
 225 230 235 240
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
 245 250 255
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
 260 265 270
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
 275 280 285
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly
 290 295 300
 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly
 305 310 315 320
 Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr

[illegible]

aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg 547
Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr
135 140 145

gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc 595
Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly
150 155 160 165

cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag 643
Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys
170 175 180

ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg 691
Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val
185 190 195

aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg 739
Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro
200 205 210

gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc 787
Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr
215 220 225

gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct 835
Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala
230 235 240 245

ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act 883
Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr
250 255 260

ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc 931
Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg
265 270 275

aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag 979
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys
280 285 290

gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg
1027
Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val
295 300 305

cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac
1075
Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn
310 315 320 325

aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg
1123
Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala
330 335 340

cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt
1171
Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val
345 350 355

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc
1219

Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile
360 365 370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag
1267

Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu
375 380 385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt
1315

Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu
390 395 400 405

gag gtt gcc atg gat gcc gtg gct acc tgt gtg ctg ttg gca gca gcg
1363

Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala
410 415 420

gag cat tac gct aac taaaagtgaac tacagcggag aca
1401

Glu His Tyr Ala Asn
425

<210> 450

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

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Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn
20 25 30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp
35 40 45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala
50 55 60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val
65 70 75 80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln
85 90 95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile
100 105 110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser
115 120 125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg
130 135 140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro
145 150 155 160

Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys
 165 170 175
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro
 180 185 190
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met
 195 200 205
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala
 210 215 220
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly
 225 230 235 240
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser
 245 250 255
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr
 260 265 270
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly
 275 280 285
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly
 290 295 300
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu
 305 310 315 320
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala
 325 330 335
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile
 340 345 350
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala
 355 360 365
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu
 370 375 380
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro
 385 390 395 400
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val
 405 410 415
 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn
 420 425

<210> 451

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1120)

<223> RXN00448

<400> 451

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                               Val Thr Thr Lys Asp
                               1                               5
att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                10                15                20
ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                25                30                35
cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                40                45                50
tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                55                60                65
ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp
                70                75                80                85
gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403
Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
                90                95                100
gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451
Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
                105                110                115
cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499
Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp
                120                125                130
agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547
Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr
                135                140                145
ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595
Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
                150                155                160                165
atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643
Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
                170                175                180
gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
                185                190                195
cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
                200                205                210

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ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser
 215 220 225

acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu
 230 235 240 245

agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile
 250 255 260

ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu
 265 270 275

caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg
 280 285 290

tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca
 1027
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser
 295 300 305

tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag
 1075
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys
 310 315 320 325

cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc
 1120
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 330 335 340

tagttttatc ggctgatgat tct
 1143

<210> 452

<211> 340

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 452

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 20 25 30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
 35 40 45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
 50 55 60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
 65 70 75 80

Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe

85	90	95
Thr Asp Val Val Ser Val Lys Thr	Ala Val Tyr Asp Ala Val Lys Ala	
100	105	110
Arg Asn Met Gln His Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr		
115	120	125
Ala Asn Ser Gly Trp Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala		
130	135	140
Val Trp Val Val Thr Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn		
145	150	155
Ser Thr Trp Ile Ser Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala		
165	170	175
Val Gly Ala Glu Val Val Pro Ser Arg Val Gly Pro His Asp Ala Ala		
180	185	190
Ala Ala Arg Val Ser His Leu Thr His Ile Leu Ala Glu Thr Leu Ala		
195	200	205
Ile Val Gly Asp Asn Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly		
210	215	220
Ser Tyr Arg Asp Ser Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val		
225	230	235
Arg Ala Met Cys Glu Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp		
245	250	255
Glu Ala Leu Ala Ile Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu		
260	265	270
Gln Pro Asn Ile Glu Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile		
275	280	285
Arg Tyr Glu Ala Arg Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser		
290	295	300
Pro Thr Ile Thr Ser Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr		
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Pro Asn Trp Glu Lys Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg		
325	330	335
Ile Glu Val Phe		
340		

<210> 453

<211> 689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(666)

<223> FRXA00448

<400> 453

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1				5					10					15		
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc	96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe	
			20					25					30			
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc	144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile	
		35					40					45				
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc	192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val	
	50					55					60					
cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat	240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His	
65					70					75					80	
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggg	gac	aac	ggg	288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly	
			85						90					95		
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc	336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr	
			100					105					110			
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc	384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser	
		115					120					125				
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc	432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu	
	130					135					140					
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa	480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln	
	145				150					155					160	
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc	528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser	
				165					170					175		
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc	576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser	
			180						185				190			
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag	624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln	
		195					200					205				
ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc			666
Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe			
	210					215					220					
tag	ttttatc	ggctgatgat	tct													689

<210> 454

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 454

Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser
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Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe
 20 25 30

Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
 35 40 45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
 50 55 60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His
 65 70 75 80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
 85 90 95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
 100 105 110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
 115 120 125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
 130 135 140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
 145 150 155 160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
 165 170 175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
 180 185 190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
 195 200 205

Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 210 215 220

<210> 455

<211> 346

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(346)

<223> FRXA00452

<400> 455

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catagagata accgtagtag gtatgtgccca cacttgtcag gtg act acc aaa gac 115
Val Thr Thr Lys Asp
1 5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
10 15 20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
25 30 35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
40 45 50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
55 60 65

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70 75 80

<210> 456

<211> 82

<212> PRT

<213> Corynebacterium glutamicum

<400> 456

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
1 5 10 15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
20 25 30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
35 40 45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
50 55 60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
65 70 75 80

Asp Ser

<210> 457

<211> 1248

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1225)

<223> RXA00584

<400> 457

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 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn
 230 235 240 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala
 250 255 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu
 265 270 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln
 280 285 290

gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa
 1027
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu
 295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag
 1075
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln
 310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg
 1123
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val
 330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc
 1171
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile
 345 350 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca
 1219
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala
 360 365 370

ccc aag taattaaggg cctagactg tta
 1248
 Ala Lys
 375

<210> 458

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
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Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu
 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys

35	40	45
Gln Ala Ser Lys Val Glu	Gln Asp Arg Gln Asp Ile	Ala Asp Ile Phe
50	55	60
Ala Gly Asp Asp Asp Arg	Leu Val Val Val Val Gly	Pro Cys Ser Val
65	70	75
His Asp Pro Glu Ala Ala Ile	Asp Tyr Ala Asn Arg Leu	Ala Pro Leu
85	90	95
Ala Lys Arg Leu Asp Gln Asp	Leu Lys Ile Val Met Arg	Val Tyr Phe
100	105	110
Glu Lys Pro Arg Thr Ile Val	Gly Trp Lys Gly Leu Ile	Asn Asp Pro
115	120	125
His Leu Asn Glu Thr Tyr Asp	Ile Pro Glu Gly Leu Arg	Ile Ala Arg
130	135	140
Lys Val Leu Ile Asn Val Val	Asn Leu Asp Leu Pro Val	Gly Cys Glu
145	150	155
Phe Leu Glu Pro Asn Ser Pro	Gln Tyr Tyr Ala Asp Thr	Val Ala Trp
165	170	175
Gly Ala Ile Gly Ala Arg Thr	Thr Glu Ser Gln Val His	Arg Gln Leu
180	185	190
Ala Ser Gly Met Ser Met Pro	Ile Gly Phe Lys Asn Gly	Thr Asp Gly
195	200	205
Asn Ile Gln Val Ala Val Asp	Ala Val Gln Ala Ala Gln	Asn Pro His
210	215	220
Phe Phe Phe Gly Thr Ser Asp	Asp Gly Ala Leu Ser Val	Val Glu Thr
225	230	235
Ala Gly Asn Ser Asn Ser His	Ile Ile Leu Arg Gly Gly	Thr Ser Gly
245	250	255
Pro Asn His Asp Ala Ala Ser	Val Glu Ala Val Val Glu	Lys Leu Gly
260	265	270
Glu Asn Ala Arg Leu Met Ile	Asp Ala Ser His Ala Asn	Ser Gly Lys
275	280	285
Asp His Ile Arg Gln Val Glu	Val Val Arg Glu Ile Ala	Glu Gln Ile
290	295	300
Ser Gly Gly Ser Glu Ala Val	Ala Gly Ile Met Ile Glu	Ser Phe Leu
305	310	315
Val Gly Gly Ala Gln Asn Leu	Asp Pro Ala Lys Leu Arg	Ile Asn Gly
325	330	335
Gly Glu Gly Leu Val Tyr Gly	Gln Ser Val Thr Asp Lys	Cys Ile Asp
340	345	350
Ile Asp Thr Thr Ile Asp Leu	Leu Ala Glu Leu Ala Ala	Ala Val Arg
355	360	365

Glu Arg Arg Ala Ala Ala Lys
370 375

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<211> 1983
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1960)
<223> RXA00579

<400> 459
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Met Arg Val Leu Ile
1 5
att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
10 15 20
gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
25 30 35
gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
40 45 50
gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
55 60 65
gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
70 75 80 85
~~ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg atc cac ggt 403~~
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly
90 95 100
gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
105 110 115
cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
120 125 130
ttg ccg gag tca ttg aaa gcc aca gct acc agc gat gat ggt ttg atc 547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
135 140 145
atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
150 155 160 165

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643
 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe
 170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His
 200 205 210

tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt 787
 Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu
 215 220 225

ggt gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc 835
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly
 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser
 250 255 260

gtt gcg ccc ggt caa ttt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931
 Val Ala Pro Gly Gln Lys Phe Arg Leu Gly Trp Val Gly Tyr Val Gly
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa
 1027
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt
 1075
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct
 1123
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro
 330 335 340

tgc tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat
 1171
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg
 1219
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc
 1267
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala

375	380	385
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Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr 390 395 400 405		
ggg gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg 1363		
Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro 410 415 420		
gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc 1411		
Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro 425 430 435		
att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa 1459		
Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu 440 445 450		
atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg 1507		
Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu 455 460 465		
atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc 1555		
Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro 470 475 480 485		
acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca 1603		
Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr 490 495 500		
gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt 1651		
Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser 505 510 515		
ccg att gag tac gtc cgc gca gca ttc ccc ggt ggt tcg atg act cgt 1699		
Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly 520 525 530		
gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct 1747		
Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala 535 540 545		
cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795		
Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly 550 555 560 565		
gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843		
Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn 570 575 580		

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt
1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu
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Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
195 200 205

Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp
 450 455 460
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala
 465 470 475 480
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val
 485 490 495
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu
 500 505 510
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly
 515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp
 530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr
 545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu
 565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu
 580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser
 595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro
 610 615 620

<210> 461
 <211> 747
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(724)
 <223> RXA00958

<400> 461

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ccattgcgct tgctgctggt tccacttttg aggtcatccg atg aca cac gtt gtt 115
 Met Thr His Val Val
 1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
 10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
 25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
 40 45 50

cct ggt tac cct gcc gat gcg gcc aac atg atg gcg ctg atc gag cgc 307
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
 55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
 70 75 80 85

ctc atc gaa tac cac gcc gcc aag gtt gag cct tgt gcc cct gtg cac 403
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
 90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451

Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
 105 110 115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
 120 125 130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
 135 140 145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
 150 155 160 165

ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
 170 175 180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
 185 190 195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 200 205

tca 747

<210> 462

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
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Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
 20 25 30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
 35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
 50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
 65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
 85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
 100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
 115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

130					135					140					
Ser	Leu	Gly	Cys	Val	Val	Ala	Pro	Asp	Gly	Ile	Glu	Ser	Leu	Gly	Thr
145					150					155					160
Cys	Ser	Ser	Glu	Ile	Gly	Asp	Val	Ile	Met	Ala	Ala	Arg	Thr	Thr	Asp
				165					170					175	
Gly	Lys	Ala	Ile	Gly	Leu	Gln	Phe	His	Pro	Glu	Ser	Val	Leu	Ser	Pro
			180					185					190		
Thr	Gly	Pro	Val	Ile	Leu	Ser	Arg	Cys	Val	Glu	Gln	Leu	Leu	Ala	Asn
		195					200					205			

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<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS  
<222> (101)..(469)  
<223> RXN03007
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Met Thr Ser Pro Ala															
1 5															
aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg															163
Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu															
10 15 20															
gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat															211
Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp															
25 30 35															
gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag															259
Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu															
40 45 50															
cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct															307
Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala															
55 60 65															
cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act															355
Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr															
70 75 80 85															
ggc ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg															403
Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu															
90 95 100															
atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg															451
Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser															

105 110 115 469

gtg agc tcc aag tcc ggc
Val Ser Ser Lys Ser Gly
120

<210> 464
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

<400> 464
Met Thr Ser Pro Ala Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn
1 5 10 15
Pro Thr Pro Thr Leu Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr
20 25 30
Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile
35 40 45
Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala
50 55 60
Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu
65 70 75 80
Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr
85 90 95
Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys
100 105 110
His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly
115 120

<210> 465
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXN02918

<400> 465
agattgtcgc ttttcccatt tctccgggtt ttctggaact ttttgggcgt atgctgggaa 60
tgattctatt attgccaaat cagaaagcag gagagaccgc atg agc gaa atc cta 115
Met Ser Glu Ile Leu
1 5
gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163
Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala
10 15 20
ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211
Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His

25	30	35	
acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc			259
Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr			
40	45	50	
gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg			307
Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala			
55	60	65	
cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg			355
Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu			
70	75	80	85
ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc			403
Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser			
90	95	100	
aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc			451
Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser			
105	110	115	
cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct			499
Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser			
120	125	130	
gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac			541
Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp			
135	140	145	
taattgtctc ccatttaagg agt			564

<210> 466

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 466

Met	Ser	Glu	Ile	Leu	Glu	Thr	Tyr	Trp	Ala	Pro	His	Phe	Gly	Lys	Thr
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Glu	Glu	Ala	Thr	Ala	Leu	Val	Ser	Tyr	Leu	Ala	Gln	Ala	Ser	Gly	Asp
		20						25					30		

Pro	Ile	Glu	Val	His	Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu
		35				40						45			

Ser	Gly	Asn	Tyr	Thr	Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe
	50					55					60				

Leu	Leu	Val	Ala	Ala	Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr
65					70					75					80

Gly	Gly	Val	Asn	Leu	Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg
			85					90						95	

Leu	His	Val	Glu	Ser	Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys
			100					105					110		

Tyr	Phe	Ala	Leu	Ser	Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125	
Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser	Glu Glu Leu Arg Gly		
130	135	140	
Gln Leu Asp			
145			
<210> 467			
<211> 735			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(712)			
<223> RXN01116			
<400> 467			
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acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt 115			
		Met Ala Ala Arg Val	
		1 5	
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg 163			
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met			
10 15 20			
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt 211			
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu			
25 30 35			
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag 259			
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu			
40 45 50			
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt 307			
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val			
55 60 65			
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc 355			
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile			
70 75 80 85			
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc 403			
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser			
90 95 100			
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag 451			
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys			
105 110 115			
ggg atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc 499			
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile			
120 125 130			
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag 547			
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys			
135 140 145			

gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val
 150 155 160 165
 acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu
 170 175 180
 atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr
 185 190 195
 gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735
 Glu Ala Asp Phe Lys Val Ala
 200

<210> 468

<211> 204

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn
 1 5 10 15
 Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly
 20 25 30
 Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro
 35 40 45
 Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys
 50 55 60
 Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp
 65 70 75 80
 Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly
 85 90 95
 Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
 100 105 110
 Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly
 115 120 125
 Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala
 130 135 140
 Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys
 145 150 155 160
 Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu
 165 170 175
 Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu
 180 185 190
 Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

195

200

<210> 469
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)
 <223> RXN01115

<400> 469
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 gccagggtct tgcagctgtc ttgaaaagg agaactaaaa atg gct att ttg cac 115
 Met Ala Ile Leu His
 1 5
 agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163
 Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser
 10 15 20
 ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211
 Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His
 25 30 35
 aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259
 Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser
 40 45 50
 gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307
 Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val
 55 60 65
 ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355
 Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly
 70 75 80 85
 cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403
 Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp
 90 95 100
 cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451
 Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu
 105 110 115
 ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499
 Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr
 120 125 130
 ggt tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547
 Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp
 135 140 145
 ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595
 Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala
 150 155 160 165
 ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643

Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr
 170 175 180

tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc 691
 Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr
 185 190 195

atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc 739
 Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile
 200 205 210

att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca 787
 Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro
 215 220 225

gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg 835
 Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu
 230 235 240 245

cta gca cag cat ttc gct taatgttgta ggcattgttca caa 876
 Leu Ala Gln His Phe Ala
 250

<210> 470

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 470

Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu
 1 5 10 15

Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln
 20 25 30

Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg
 35 40 45

Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp
 50 55 60

Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn
 65 70 75 80

Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu
 85 90 95

Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala
 100 105 110

Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys
 115 120 125

Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp
 130 135 140

Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe
 145 150 155 160

Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys

	165		170		175
Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr					
	180		185		190
Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro					
	195		200		205
Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala					
	210		215		220
Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn					
	225		230		235
Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala					
	245		250		

<210> 471
 <211> 1284
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1261)
 <223> RXS00116

<400> 471
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 tttgcgcacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115
 Met Ser Asn Asp Phe
 1 5
 gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
 Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
 10 15 20
 acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
 Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
 25 30 35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259
 Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
 40 45 50
 att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307
 Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
 55 60 65
 ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355
 Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
 70 75 80 85
 tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403
 Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
 90 95 100
 att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451
 Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile

105	110	115	
gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg			499
Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala			
120	125	130	
ggg gcg acg cgg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg			547
Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp			
135	140	145	
gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg cgg			595
Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg			
150	155	160	165
atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct			643
Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser			
170	175	180	
aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg			691
Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu			
185	190	195	
ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag			739
Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln			
200	205	210	
aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg			787
Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val			
215	220	225	
acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg			835
Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr			
230	235	240	245
ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg			883
Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala			
250	255	260	
aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg			931
Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val			
265	270	275	
gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag			979
Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys			
280	285	290	
ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg			
1027			
Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala			
295	300	305	
ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat			
1075			
Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp			
310	315	320	325
att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag			
1123			
Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys			
330	335	340	

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
1171

Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
345 350 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
1219

Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
360 365 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
1261

Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
375 380 385

tagtttgaac aggttggttg ggg
1284

<210> 472

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr
1 5 10 15

Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn
20 25 30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
130 135 140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
145 150 155 160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
165 170 175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
180 185 190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
 195 200 205
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
 210 215 220
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
 225 230 235 240
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
 245 250 255
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
 260 265 270
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
 275 280 285
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
 290 295 300
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
 305 310 315 320
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
 355 360 365
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
 370 375 380
 Lys Lys Leu
 385

<210> 473

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 473

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ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115
 Met Thr Gln Arg Ala
 1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
 10 15 20

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
 25 30 35

aat aat cag tat tct gcg ggg cgt ggg gat gct tct ttg agg gca gct 259
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
 40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
 55 60 65

tct gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
 70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
 90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
 105 110 115

gtg gcg gtt cct ttg cag gag gtg gag aac tct tgg gat gtg gat gtc 499
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
 120 125 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
 135 140 145

aat tct ccg cat aat ccg acg ggt tct gtg ttt tct aag aag gcg ttg 595
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
 150 155 160 165

aag cag ttg gcg 607
 Lys Gln Leu Ala

<210> 474

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly
 1 5 10 15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65 70 75 80

ctc agc aca ggt ttt cac att gac gct ttc gca ggc gcc gcg gca gaa 403
Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala Gly Ala Ala Glu
90 95 100

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

tgc 843

<210> 476

<211> 240

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
 1 5 10 15

Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
 20 25 30

Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
 35 40 45

Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
 50 55 60

Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
 65 70 75 80

Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

85	90	95
Gly Ala Ala Ala Glu Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser 100	105	110
Leu Thr Pro Met Gln Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile 115	120	125
Glu Ala Leu Lys Leu Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu 130	135	140
Ser Lys Gln Ala Arg Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val 145	150	155
Thr Thr Tyr Gly Ser Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly 165	170	175
Lys Pro Ile Pro Gly Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu 180	185	190
Leu Gly Gly Pro Met Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His 195	200	205
Pro Asp Phe Ala Asn Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu 210	215	220
Leu His Asp Gly Ile Leu Thr Val Thr Gly Arg Val Asp Thr Arg His 225	230	235
		240

<210> 477
 <211> 1017
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(994)
 <223> RXS00393

<400> 477
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 aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat	307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg	835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
 1017
 Ala Leu Ala Phe Ser
 295

<210> 478
 <211> 298
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 478
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
 1 5 10 15
 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

260 265 270
 Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala
 275 280 285
 Val Leu Thr Gly Leu Ala Leu Ala Phe Ser
 290 295

<210> 479
 <211> 1005
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(982)
 <223> FRXA00393

<400> 479
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 aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65
~~tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355~~
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100
 gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
 105 110 115
 ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
 120 125 130
 ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
 135 140 145

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ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
150                155                160                165

gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
170                175                180

gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
185                190                195

aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
200                205                210

gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
215                220                225

att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
230                235                240

cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
250                255                260

ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tgc 931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
265                270                275

gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
280                285                290

cat tagcgttttag ctaaaacgct ttt
1005
His

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<210> 480

<211> 294

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 480

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Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
  1                5                10                15

Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
20                25                30

Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
35                40                45

Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
50                55                60

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Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp
 260 265 270
 Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro
 275 280 285
 Cys Ser Arg Ala Trp His
 290

<210> 481
 <211> 987
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(964)
 <223> RXS00446

<400> 481
 tgctacgaag ttatctagta atgaagttag tttttccct ctcccggcag cagttgatgc 60
 ggtgacggag gctacttggg gggctaatacg gtaccggat atg ggt gcg gtt gag 115
 Met Gly Ala Val Glu

	1	5	
ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc			163
Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val			
	10	20	
acg gta ggt tgc ggc tcg tct gcg ctg tgt caa cag ctg gtt cag gca			211
Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln Gln Leu Val Gln Ala			
	25	35	
acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag			259
Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu			
	40	50	
gct tat cca att ttc gcg cag gtc gcg ggc gcc act cct gtt gcc att			307
Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala Thr Pro Val Ala Ile			
	55	65	
ccg ctg act gct gat cag aat cat gat ctt gat gcg atg gca gcc gcg			355
Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp Ala Met Ala Ala Ala			
	70	85	
atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct			403
Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro			
	90	100	
tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag			451
Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys			
	105	115	
gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc			499
Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe			
	120	130	
aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac			547
Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His			
	135	145	
gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg			595
Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala			
	150	165	
ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg			643
Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala			
	170	180	
atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg			691
Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala			
	185	195	
gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg			739
Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val			
	200	210	
gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct			787
Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala			
	215	225	
gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct			835
Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala			
	230	245	

tgc	987
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<213> Corynebacterium glutamicum

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
100 105 110

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu
195 200 205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val
 210 215 220

Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro
 225 230 235 240

Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile
 245 250 255

Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala
 260 265 270

Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 275 280 285

<210> 483

<211> 545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(522)

<223> FRXA00446

<400> 483

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 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 5 10 15

ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Ile
 20 25 30

cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

tagtctttgg cgttttgagg tgc 545

<210> 484

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 5 10 15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

<210> 485

<211> 1230

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1207)

<223> RXS00618

<400> 485

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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
                                         Met Gln Met Leu Asp
                                         1           5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10                        15                        20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25                        30                        35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40                        45                        50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55                        60                        65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                        70                        75                        80                        85

ggg gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
                        90                        95                        100

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
                        105                        110                        115

tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
                        120                        125                        130

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
                        135                        140                        145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
                        150                        155                        160                        165

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
                        170                        175                        180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
                        185                        190                        195

ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739

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Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr
 200 205 210
 ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
 215 220 225
 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
 230 235 240 245
 tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
 250 255 260
 act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
 265 270 275
 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
 280 285 290
 act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct
 1027
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
 295 300 305
 gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa
 1075
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
 310 315 320 325
 gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc
 1123
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
 330 335 340
 cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att
 1171
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
 345 350 355

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 360 365

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 1230

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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
 85 90 95
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
 100 105 110
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
 115 120 125
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
 130 135 140
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
 145 150 155 160
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
 165 170 175
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
 180 185 190
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
 195 200 205
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
 210 215 220
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
 225 230 235 240
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
 245 250 255
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
 260 265 270
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
 275 280 285
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
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 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
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 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
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340 345 350
 Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
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Lys

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 Met Ser Phe Gly Arg
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 ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163
 Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly
 10 15 20
 acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211
 Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile
 25 30 35
 atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259
 Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser
 40 45 50
 ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307
 Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala
 55 60 65
~~ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac att gaa ggc tat 355~~
 Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr
 70 75 80 85
 cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403
 Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu
 90 95 100
 ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451
 Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val
 105 110 115
 tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499
 Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp
 120 125 130
 gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547
 Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu
 135 140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
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<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

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 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
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Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
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Lys Lys

<210> 489

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> FRXA00627

<400> 489

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				1				5	

cga	gtc	cac	cgt	cgc	agg	cgc	gaa	ggc	aaa	gac	acc	tta	atg	ttc	tgc	163
Arg	Val	His	Arg	Arg	Arg	Arg	Glu	Gly	Lys	Asp	Thr	Leu	Met	Phe	Cys	
			10					15						20		

gct	ggc	cag	ccg	tca	act	ggg	gcg	cca	gaa	gca	gtc	atc	gaa	gaa	gca	211
Ala	Gly	Gln	Pro	Ser	Thr	Gly	Ala	Pro	Glu	Ala	Val	Ile	Glu	Glu	Ala	
			25					30					35			

gag	atc	gct	ctt	cgc	tcg	ggg	cct	ttg	gga	tac	acc	gag	gtg	att	ggg	259
Glu	Ile	Ala	Leu	Arg	Ser	Gly	Pro	Leu	Gly	Tyr	Thr	Glu	Val	Ile	Gly	
		40					45					50				

gat	cgt	gag	ttc	cgt	gaa	cgc	atc	gcc	gat	tgg	cac	tct	gct	act	tat	307
Asp	Arg	Glu	Phe	Arg	Glu	Arg	Ile	Ala	Asp	Trp	His	Ser	Ala	Thr	Tyr	
	55					60					65					

gac	gta	gac	acc	aac	cct	gac	aat	gtt	att	gtc	acc	acc	ggg	tct	tca	355
Asp	Val	Asp	Thr	Asn	Pro	Asp	Asn	Val	Ile	Val	Thr	Thr	Gly	Ser	Ser	
	70				75					80					85	

ggg	gga	ttc	gtg	gca	tcg	ttt	atc	gcc	acc							385
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				90				95								

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<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 490

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Val	Ile	Glu	Glu	Ala	Glu	Ile	Ala	Leu	Arg	Ser	Gly	Pro	Leu	Gly	Tyr
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Thr	Glu	Val	Ile	Gly	Asp	Arg	Glu	Phe	Arg	Glu	Arg	Ile	Ala	Asp	Trp
	50					55					60				

His	Ser	Ala	Thr	Tyr	Asp	Val	Asp	Thr	Asn	Pro	Asp	Asn	Val	Ile	Val
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Thr	Thr	Gly	Ser	Ser	Gly	Gly	Phe	Val	Ala	Ser	Phe	Ile	Ala	Thr	
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 <223> RXS01105

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 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
 10 15 20
 ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
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 cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
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 gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
 Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
 55 60 65
 gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
 Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
 70 75 80 85
 gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
 Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
 90 95 100
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 Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
 105 110 115
 gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
 120 125 130
 cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
 His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
 135 140 145
 atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595
 Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val
 150 155 160 165
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 Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp
 170 175 180

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
 Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
 185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739
 Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu
 200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787
 Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala
 215 220 225

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 Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala
 230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883
 Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala
 250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931
 Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr
 265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979
 Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala
 280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt
 1027
 Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe
 295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt
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 Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu
 330 335 340

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 1171
 Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala
 345 350 355

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 Ala Ala Glu Ile Ile Lys Leu Asn Leu
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tga
 1221

<210> 492
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 492

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Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
          35           40           45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
          50           55           60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
          65           70           75           80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
          85           90           95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
          100          105          110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
          115          120          125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
          130          135          140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
          145          150          155          160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
          165          170          175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
          180          185          190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
          195          200          205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
          210          215          220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
          225          230          235          240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
          245          250          255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
          260          265          270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
          275          280          285

Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
          290          295          300

Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
          305          310          315          320

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Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1729)

<223> RXS02315

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Met Ser Ser Thr Pro
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gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
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act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tgc ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
55 60 65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
105 110 115

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Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
120 125 130

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Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu Ser Leu Ala Gln Gly
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 Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala Leu Asp Val Pro Leu
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 gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643
 Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu Ala Val Gly Ala Ser
 170 175 180
 tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691
 Trp Thr His Arg Trp Ile Asn His Gly Glu Val Thr Val Asp Leu Gly
 185 190 195
 gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739
 Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala Trp Glu Val Glu Gly
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 Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr Ala Pro Lys Pro Tyr
 215 220 225
 aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc 835
 Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu Leu Lys Glu Gln Val
 230 235 240 245
 tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg 883
 Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro Asp His Val Ile Val
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 gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat 931
 Val Gly His Pro Thr Leu His Arg Gly Val Leu Lys Leu Met Ser Asp
 265 270 275
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 Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr Asp Ile Ile Thr Asp
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 Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr Val Lys Val Thr Gly
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 gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc
 1123
 Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn Gln Glu Phe Gly Phe
 330 335 340
 acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc
 1171
 Thr Gly Leu His Val Ala Ala Ala Val Ala Asp Thr Leu Gly Thr Gly
 345 350 355
 gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg
 1219

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu
360 365 370

gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc
1267

Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val
375 380 385

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1315

Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala
390 395 400 405

gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc
1363

Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala
410 415 420

ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc
1411

Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
425 430 435

ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
1459

Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
440 445 450

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1507

Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
455 460 465

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1555

Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
470 475 480 485

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1603

Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
490 495 500

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1651

Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
505 510 515

gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca
1699

Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
520 525 530

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1749

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1752

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<211> 543

<212> PRT

<213> Corynebacterium glutamicum

<400> 494

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 35 40 45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
 50 55 60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
 65 70 75 80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
 85 90 95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
 100 105 110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
 115 120 125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
 130 135 140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
 145 150 155 160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
 165 170 175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
 180 185 190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
 195 200 205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
 210 215 220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
 225 230 235 240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
 245 250 255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
 260 265 270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
 275 280 285

Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290 295 300
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305 310 315 320
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
 325 330 335
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
 340 345 350
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355 360 365
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
 370 375 380
 Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
 385 390 395 400
 Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
 405 410 415
 Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
 420 425 430
 Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
 435 440 445
 Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
 450 455 460
 Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
 465 470 475 480
 Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
 485 490 495
 His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
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 Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
 515 520 525

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<210> 495

<211> 1434

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1411)

<223> RXS02550

<400> 495

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	Val Thr Thr Asp Lys	
	1 5	
cgc aaa acc tct aag acc acc gac acc gcc aac aag gct gtg ggc gcg	163	
Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn Lys Ala Val Gly Ala		
	10 15 20	
gat cag gca gcg cgt ccc act cgg cga aca act cgc cgc atc ttc gat	211	
Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr Arg Arg Ile Phe Asp		
	25 30 35	
cag tcg gag aag atg aag gac gtg ctg tac gag atc cgt ggc ccg gtg	259	
Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu Ile Arg Gly Pro Val		
	40 45 50	
gcc gcg gag gcg gaa cgc atg gag ctt gat ggg cat aac atc tta aag	307	
Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly His Asn Ile Leu Lys		
	55 60 65	
ctc aac acg gga aat cca gcc gtg ttc gga ttc gat gcc ccc gac gtg	355	
Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe Asp Ala Pro Asp Val		
	70 75 80 85	
att atg cgt gac atg atc gcc aac ctt cca act tcc caa ggg tat tcc	403	
Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr Ser Gln Gly Tyr Ser		
	90 95 100	
acc tcc aaa ggc att att ccg gcc cgg cga gca gtg gtc acc cgc tac	451	
Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala Val Val Thr Arg Tyr		
	105 110 115	
gaa gtt gtg ccc gga ttc ccc cac ttc gat gtt gat gat gtg ttc tta	499	
Glu Val Val Pro Gly Phe Pro His Phe Asp Val Asp Asp Val Phe Leu		
	120 125 130	
ggc aac ggt gtc tca gaa cta atc acc atg acc acc caa gca ctc ctc	547	
Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr Thr Gln Ala Leu Leu		
	135 140 145	
aac gac ggc gat gaa gtt ctt atc ccc gca ccg gac tac cca ctg tgg	595	
Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro Asp Tyr Pro Leu Trp		
	150 155 160 165	
act gcc gca acc tcc ctg gct ggt ggt aag cct gtg cac tac ctc tgt	643	
Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro Val His Tyr Leu Cys		
	170 175 180	
gat gag gaa gat gac tgg aac cca tcc atc gaa gac atc aag tcc aaa	691	
Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu Asp Ile Lys Ser Lys		
	185 190 195	
atc tca gag aaa acc aaa gct att gtg gtg atc aac ccc aac aac ccc	739	
Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile Asn Pro Asn Asn Pro		
	200 205 210	
acg gga gct gtc tac ccg cgc cgg gtg ttg gaa caa atc gtc gag att	787	
Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu Gln Ile Val Glu Ile		
	215 220 225	

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835
 Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc
 1027
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga
 1075
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa
 1123
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc
 1171
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc
 1219
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc
 1267
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca
 1315
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg
 1363
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag
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1434

<210> 496

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

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			20					25					30		
Arg	Arg	Ile	Phe	Asp	Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	Tyr	Glu
		35					40					45			
Ile	Arg	Gly	Pro	Val	Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	Asp	Gly
	50					55					60				
His	Asn	Ile	Leu	Lys	Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	Gly	Phe
65					70					75					80
Asp	Ala	Pro	Asp	Val	Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	Pro	Thr
				85					90					95	
Ser	Gln	Gly	Tyr	Ser	Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	Arg	Ala
		100						105					110		
Val	Val	Thr	Arg	Tyr	Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	Asp	Val
		115					120					125			
Asp	Asp	Val	Phe	Leu	Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	Met	Thr
	130					135					140				
Thr	Gln	Ala	Leu	Leu	Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	Ala	Pro
145					150					155					160
Asp	Tyr	Pro	Leu	Trp	Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	Lys	Pro
			165						170					175	
Val	His	Tyr	Leu	Cys	Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	Glu
			180					185					190		
Asp	Ile	Lys	Ser	Lys	Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile
		195					200					205			
Asn	Pro	Asn	Asn	Pro	Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	Leu	Glu
	210					215					220				
Gln	Ile	Val	Glu	Ile	Ala	Arg	Glu	His	Asp	Leu	Leu	Ile	Leu	Ala	Asp
225					230					235					240
Glu	Ile	Tyr	Asp	Arg	Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu
			245						250					255	
Ala	Thr	Leu	Ala	Pro	Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser
		260						265					270		

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
 275 280 285
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
 290 295 300
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
 305 310 315 320
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
 325 330 335
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
 405 410 415
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
 420 425 430
 Ser Thr Tyr Lys Gln
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<210> 497
 <211> 1080
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1057)
 <223> RXS02319

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 agaccttgga catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115
 Met Ser Asn Tyr Ser
 1 5
 acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
 10 15 20
 gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
 25 30 35
 gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn

40	45	50	
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65			307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85			355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100			403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115			451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
ggc ggc cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180			643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195			691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290			979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
310 315

aaa
1080

<210> 498

<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 498

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20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210	215	220	
Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp			
225	230	235	240
His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn			
	245	250	255
Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu			
	260	265	270
Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr			
	275	280	285
Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe			
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Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr			
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Leu Lys Leu His Pro 5			
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163			
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala 20			
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211			
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala 35			
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259			
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp 50			
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307			
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser 65			
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355			
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys 85			
ctg ttt tagtcttcat tcttgctggc tgc 384			
Leu Phe			

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 <211> 87
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 500
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 20 25 30
 Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
 35 40 45
 Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
 50 55 60
 Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
 65 70 75 80
 Arg Ala Ile Ala Lys Leu Phe
 85

<210> 501
 <211> 775
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(775)
 <223> RXS03003

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 Met Thr Ser Arg Thr
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
 10 15 20
 gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
 25 30 35
 gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
 40 45 50
 gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
 55 60 65
 gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355

Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
 70 75 80 85
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145
 atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
 200 205 210
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
 215 220 225

<210> 502

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 502

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 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
 50 55 60
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80

<400> 503
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724

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 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg
 70 75 80 85
 ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390
 Phe Trp Met Leu

<210> 504
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 504
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 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
 35 40 45
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
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 65 70 75 80
 Thr Leu Arg Trp Arg Phe Trp Met Leu
 85

<210> 505
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(598)
 <223> RXS03074

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 tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50
 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65
 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85
 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100
 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115
 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130
 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145
 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165
 cag taatttggtt tgacgacgca gta 621
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<210> 506

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 506

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 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45
 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60
 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80
 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
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<210> 507
 <211> 3075
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(3052)
 <223> RXC01434

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 Val Leu Gly Ala Val
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
 10 15 20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
 25 30 35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met
 55 60 65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
 70 75 80 85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys
 90 95 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
 105 110 115

ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag 499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln
120 125 130

gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc 547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr
135 140 145

ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc 595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg
150 155 160 165

gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag 643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys
170 175 180

caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc 691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser
185 190 195

cag ttc ggt tac atc acc act cgc att gcg tgg att gca gac gat 739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp
200 205 210

gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct 787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro
215 220 225

tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg 835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu
230 235 240 245

tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt 883
Ser Arg Asn Ala Ala Asp Gly Asp Arg Ala Val Val Ser Asp Leu
250 255 260

cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg 931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val
265 270 275

ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac 979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr
280 285 290

ggc caa ttc gat gcc aac gcc aac atc ctt ggt tgg act ctg agc
1027

Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser
295 300 305

ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg
1075
Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu
310 315 320 325

cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc
1123
Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile
330 335 340

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gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg
 1171
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac
 1219
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc
 1267
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg
 1315
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg
 1363
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Trp Ala Leu
 410 415 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta
 1411
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc
 1459
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc
 1507
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt
 1555
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag
 1603
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc
 1651
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg
 1699
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat
1747

Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc
1795

His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc
1843

Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag
1891

Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta
1939

Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg
1987

Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt
2035

Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc
2083

Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag
2131

Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
665 670 675

tgc cga att cgt acc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg
2179

Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc
2227

Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc
2275

Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
710 715 720 725

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aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc
 2323
 Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro 740
 730

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc
 2371
 Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr 755
 745

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct
 2419
 Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro 770
 760

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg
 2467
 Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met 785
 775

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc
 2515
 Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala 805
 790 795 800

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa
 2563
 Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln 820
 810 815

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct
 2611
 Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro 835
 825 830

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat
 2659
 Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp 850
 840 845

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc
 2707
 Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser 865
 855 860

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc
 2755
 Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser 885
 870 875 880

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc
 2803
 Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser 900
 890 895

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc
 2851
 Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala 915
 905 910

tca cca cac tcc ctg tcc gaa ggc atc gag atc ggc acc gtg gat tat
2899

Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg
2947

Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca
2995

Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt
3043

Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac
3075

Val Gly Trp

<210> 508

<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

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Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu
20 25 30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile
35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
145 150 155 160

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Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
 245 250 255
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
 260 265 270
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
 290 295 300
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
 305 310 315 320
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser

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<210> 509
<211> 930
<212> DNA
<213> Corynebacterium glutamicum
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<400> 509
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Met Ser Ile Glu Trp
1 5

tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163
Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala
10 15 20

gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct 211
Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro
25 30 35

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att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac	259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
40 45 50	
acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
90 95 100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
120 125 130	
act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
150 155 160 165	
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg	643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
170 175 180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa	691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata	739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
200 205 210	
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg	787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga	835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
250 255 260	
acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc	930
Thr Val Ile Val Met Thr Ile Gly	
265	

<210> 510
 <211> 269
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 510
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 20 25 30
 Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
 35 40 45
 Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
 50 55 60
 Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
 65 70 75 80
 Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
 85 90 95
 Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
 100 105 110
 Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
 115 120 125
 His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
 130 135 140
 Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
 145 150 155 160
 Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
 165 170 175
 Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
 180 185 190
 Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
 195 200 205
 Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
 210 215 220
 Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
 225 230 235 240
 Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
 245 250 255
 Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
 260 265

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<213> Corynebacterium glutamicum

<220>

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<222> (101)..(646)

<223> RXC02789

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ttcttaacac	taaacaatgg	aaaggtaagc	gggtttttct	atg	aag	ggt	tcc	gcc	115
				Met	Lys	Val	Ser	Ala	
				1				5	

gat	aca	ccc	ggt	cac	gat	gat	cca	ggc	cca	ggc	cgg	cgc	ctt	ggc	tta	163
Asp	Thr	Pro	Gly	His	Asp	Asp	Pro	Gly	Pro	Gly	Arg	Arg	Leu	Gly	Leu	
			10					15						20		

gat	gtc	ggc	acc	gtg	cgc	atc	gga	gtg	gca	gcc	tct	gac	cgc	gat	gcc	211
Asp	Val	Gly	Thr	Val	Arg	Ile	Gly	Val	Ala	Ala	Ser	Asp	Arg	Asp	Ala	
			25					30						35		

aag	ctt	gcc	atg	cct	gtg	gaa	acc	gtt	ccg	cgg	gaa	act	gga	ttc	aaa	259
Lys	Leu	Ala	Met	Pro	Val	Glu	Thr	Val	Pro	Arg	Glu	Thr	Gly	Phe	Lys	
		40				45					50					

ggg	cca	gac	ctg	gcc	gat	att	gat	cgg	ttg	gtc	gcc	atc	gtt	gag	gaa	307
Gly	Pro	Asp	Leu	Ala	Asp	Ile	Asp	Arg	Leu	Val	Ala	Ile	Val	Glu	Glu	
	55					60					65					

tac	aac	gcc	gtg	gaa	gtc	att	gtt	ggt	cta	ccc	aca	gat	ctg	cag	gga	355
Tyr	Asn	Ala	Val	Glu	Val	Ile	Val	Gly	Leu	Pro	Thr	Asp	Leu	Gln	Gly	
	70				75				80					85		

aat	ggc	tcc	gcc	agt	gtg	aag	cat	gca	aag	gaa	att	gct	ttc	cgc	gtc	403
Asn	Gly	Ser	Ala	Ser	Val	Lys	His	Ala	Lys	Glu	Ile	Ala	Phe	Arg	Val	
				90				95						100		

cgt	cgg	cgc	ctc	acc	aat	gct	gga	aag	aac	att	ccg	gta	cgg	ctt	ggc	451
Arg	Arg	Arg	Leu	Thr	Asn	Ala	Gly	Lys	Asn	Ile	Pro	Val	Arg	Leu	Gly	
			105				110						115			

gac	gaa	aga	cta	acc	acc	gtc	gtg	gac	acc	caa	gcc	ttg	cgg	gcc	tca	499
Asp	Glu	Arg	Leu	Thr	Thr	Val	Val	Ala	Thr	Gln	Ala	Leu	Arg	Ala	Ser	
			120				125					130				

gga	gtc	agc	gaa	aaa	gcg	gga	cgt	aaa	gtt	att	gat	caa	gct	gcc	gca	547
Gly	Val	Ser	Glu	Lys	Ala	Gly	Arg	Lys	Val	Ile	Asp	Gln	Ala	Ala	Ala	
			135			140					145					

gta	gaa	atc	ctt	caa	acc	tgg	ttg	gat	gct	cgc	acc	cga	gcc	ctt	gaa	595
Val	Glu	Ile	Leu	Gln	Thr	Trp	Leu	Asp	Ala	Arg	Thr	Arg	Ala	Leu	Glu	
	150				155				160					165		

cca	caa	tcc	aca	gac	acc	caa	gat	ttc	gac	gag	aag	gga	aat	ttc	cca	643
Pro	Gln	Ser	Thr	Asp	Thr	Gln	Asp	Phe	Asp	Glu	Lys	Gly	Asn	Phe	Pro	
				170				175						180		

gga	tgaaccaa	at	ccgaaaccgc	cgg	669
Gly					

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Arg Arg Leu Gly Leu Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala
  20              25              30
Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
  35              40              45
Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
  50              55              60
Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
  65              70              75              80
Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
  85              90              95
Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
  100             105             110
Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
  115             120             125
Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile
  130             135             140
Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg
  145             150             155             160
Thr Arg Ala Leu Glu Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu
  165             170             175
Lys Gly Asn Phe Pro Gly
  180

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Met Gly Leu Glu Leu
1 5
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gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga	163
Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	
10 15 20	
tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg	211
Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu	
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc	259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg	307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg	355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att	403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt	451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	
105 110 115	
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa	499
Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga	547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc	595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc	643
Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asp Phe Leu Ser Ser	
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta	691
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg	739
Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg	787
Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt	835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	
230 235 240 245	

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880
 Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met
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tagataagtc ggggcaaact cta 903

<210> 514

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

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 20 25 30

Val Leu Ile Pro Leu Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val
 35 40 45

Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser
 50 55 60

Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu
 65 70 75 80

Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu
 85 90 95

Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val
 100 105 110

Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly
 115 120 125

Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala
 130 135 140

Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro
 145 150 155 160

Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln
 165 170 175

Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr
 180 185 190

Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp
 195 200 205

Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu
 210 215 220

Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala
 225 230 235 240

Leu Leu Thr Leu Val Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln
 245 250 255

Ile Gln Gly Met
260

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<211> 1132
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1132)
<223> RXN03063

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acctagacaa cagtttgtat ctcacctcac aggaggaacc gtg gaa gat ctc tca 115
Val Glu Asp Leu Ser
1 5

tac cgc atc ccg cag tgc cgc acc gtg gcc gag cag gtg cca ggg ccg 163
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro
10 15 20

aag tgc aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala
25 30 35

ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile
40 45 50

ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile
55 60 65

gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val
70 75 80 85

ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro
90 95 100

tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro
105 110 115

ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala
120 125 130

gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala
135 140 145

gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met
150 155 160 165

gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643
 Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu
 170 175 180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691
 Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly
 185 190 195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739
 Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser
 200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787
 Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln
 215 220 225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835
 Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile
 230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883
 Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile
 250 255 260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931
 Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu
 265 270 275

ggt gtg atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979
 Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly
 280 285 290

atg cca cta tcc gca gtg acc ggc cgc gca gaa atc atg gac gca ccc
 1027
 Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro
 295 300 305

ggc ccc ggc gcg ctc ggc gga acc tac ggc gga aac ccc gtt gct tgc
 1075
 Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys
 310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag
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 Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu Gln Ala Asp Leu Lys
 330 335 340

acc cgc gcg
 1132
 Thr Arg Ala

<210> 516

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 516

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 Ala Val Ala Arg Ala Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp
 35 40 45
 Ala Asp Gly Gly Ile Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp
 50 55 60
 Leu Ala Ser Gly Ile Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala
 65 70 75 80
 Val Ala Lys Ala Val Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys
 85 90 95
 Phe Met Val Ser Pro Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu
 100 105 110
 Asn Ala Leu Thr Pro Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn
 115 120 125
 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr
 130 135 140
 Thr Gly Lys Gly Ala Val Val Val Phe Asp Asn Ala Tyr His Gly Arg
 145 150 155 160
 Thr Asn Leu Thr Met Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser
 165 170 175
 Gly Phe Gly Pro Leu Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr
 180 185 190
 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile
 195 200 205
 Ser Val Ile Glu Ser Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val
 210 215 220
 Ile Glu Pro Ile Gln Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly
 225 230 235 240
 Phe Leu Ala Ala Ile Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe
 245 250 255
 Ile Ala Asp Glu Ile Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe
 260 265 270
 Ala Ser Asp Ala Glu Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys
 275 280 285
 Gly Ile Ala Gly Gly Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu
 290 295 300
 Ile Met Asp Ala Pro Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly
 305 310 315 320
 Asn Pro Val Ala Cys Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu
 325 330 335

Gln Ala Asp Leu Lys Thr Arg Ala
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<211> 1491
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<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1468)
<223> RXN02970

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Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tgc gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
 170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
 Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
 185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
 Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
 200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc ggc aag
 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390 395 400 405

ttc aag gaa cgc gcc gtg tgg ccg atg atc tcc gcc aac cga ttc cac
1363

Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
440 445 450

gcg ttg ttc taagttttct agataacaag gcc
1491

Ala Leu Phe
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<210> 518

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

145		150		155		160
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg	165		170		175	
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro	180		185		190	
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys	195		200		205	
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala	210		215		220	
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly	225		230		235	240
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys		245		250		255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe	260		265		270	
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe	275		280		285	
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala	290		295		300	
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly	305		310		315	320
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala		325		330		335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile		340		345		350
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu		355		360		365
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile	370		375		380	

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala	385		390		395		400
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser		405		410		415	
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu		420		425		430	
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 Leu Ala Leu Lys Gly
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 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
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 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85
 tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
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 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
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 tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130
 gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
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 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
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 tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
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Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
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cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggg	gct	ggc	atg	atc	gca	gcg	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
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Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
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Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
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ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
			265					270						275			
ctg	ttt	gct	tac	gag	cat	gct	ggc	gac	gat	ttc	cag	cca	gac	atg	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile		
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gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct		
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cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa		
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1267																	
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 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
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 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
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 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
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 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
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Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
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Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
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Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
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Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
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<223> RXA01551

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 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala
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 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly
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gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259
 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser
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ccc atc cgc aag gac ggt ctc gag gtc ccg gag acc gaa atc cgc ctc 307

Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu Thr Glu Ile Arg Leu
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 Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu Pro Arg Leu Arg Glu
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 Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met Arg Arg Gly Gln Ala
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 Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro Leu Lys Ala Leu Pro
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 Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg Ala Gly Val Ile Thr
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 Arg Glu Met Glu Phe Val Ala Leu Arg Glu His Val Asp Ala Glu Phe
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 gtg cgc tct gag gtg gcg cgc ggt cgg gcc att att ccc aac aac gtc 691
 Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile Ile Pro Asn Asn Val
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 aac cac ccc gaa tct gaa ccg atg att att ggt cgc aaa ttt ttg acc 739
 Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly Arg Lys Phe Leu Thr
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 Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val Thr Ser Ser Ile Glu
 215 220 225
 gaa gag gtg tcc aag ctg cag tgg gcc acg cgc tgg ggt gcc gat acc 835
 Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg Trp Gly Ala Asp Thr
 230 235 240 245
 gtg atg gat cta tcc acc ggc gat gat att cac acc acc cgc gaa tgg 883
 Val Met Asp Leu Ser Thr Gly Asp Asp Ile His Thr Thr Arg Glu Trp
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 Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr Val Pro Ile Tyr Gln
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Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met
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Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile Pro Leu Thr Thr Arg
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cgt gtc acc ggc att gtc tcc cgc ggc gga tcc att atg gcc ggt tgg
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Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser Ile Met Ala Gly Trp
 330 335 340

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Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr Glu His Phe Asp Glu
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Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala Phe Ser Leu Gly Asp
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 1267

Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe
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gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac
 1315

Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr
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 1363

Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met
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 1411

Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro
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 1459

Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp
 440 445 450

cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc
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His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr
 455 460 465

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 1555

Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn
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 1603

Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His

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 Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu
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 Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro
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 Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly
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 Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser
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 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu
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 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr
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 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met
 115 120 125
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro
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 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His
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 180 185 190
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly
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 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val
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 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg
 225 230 235 240
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His
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 260 265 270
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asn
 275 280 285
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln
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 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile
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 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser
 325 330 335
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr
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 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala
 355 360 365
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn

370 375 380
 Asp Ala Ala Gln Phe Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln
 385 390 395 400
 Arg Ala Trp Glu Tyr Asp Val Gln Val Met Val Glu Gly Pro Gly His
 405 410 415
 Val Pro Leu Asn Met Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp
 420 425 430
 Ala Ala Asp Ala Pro Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile
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 Ala Pro Gly Tyr Asp His Ile Thr Ser Ala Ile Gly Ala Ala His Ile
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 Ala Met Gly Gly Thr Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His
 465 470 475 480
 Leu Gly Leu Pro Asn Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr
 485 490 495
 Lys Leu Ala Ala His Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala
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 Arg Ala Trp Asp Asp Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp
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<400> 523

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Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His	
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Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala	
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Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln	
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Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	
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Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	
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Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	
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Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	
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Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	
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Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	
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 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300

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 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320

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 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

aat
 1013

<210> 524
 <211> 330
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 524
 Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro
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 Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
 20 25 30

 Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
 35 40 45

 Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
 50 55 60

 Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
 65 70 75 80

 Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
 85 90 95

 Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
 100 105 110

 Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
 115 120 125

 Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
 130 135 140

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu
 145 150 155 160

Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly
 165 170 175

Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly
 180 185 190

Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys
 195 200 205

Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly
 210 215 220

Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn
 225 230 235 240

Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255

Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270

Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285

Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300

Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320

Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

<210> 525

<211> 706

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXA01352

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ctggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115
 Val Phe Glu Asn Arg
 1 5

ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu
 10 15 20

gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25	30	35	
cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca			259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala			
40	45	50	
tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg			307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val			
55	60	65	
ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga			355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly			
70	75	80	85
ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt			403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu			
90	95	100	
gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act			451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr			
105	110	115	
gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg			499
Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu Leu Ser Asp Val Leu			
120	125	130	
gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca			547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser			
135	140	145	
ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg			595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu			
150	155	160	165
tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg			643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val			
170	175	180	
cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct			691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala			
185	190	195	
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Phe Ser Glu Ser Asp			
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<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 526

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Gly	Ser	Val	Asp	Glu	Val	Val	His	Thr	Ala	Ser	Ala	Ala	Ala	Arg	Gly
				20				25						30	

Gly	Ala	Gly	Val	Val	Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala
		35				40						45			

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser
 50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser
 65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp
 85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile
 100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu
 115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr
 130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro
 145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val
 165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val
 180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp
 195 200

<210> 527

<211> 944

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(921)

<223> RXA01381

<400> 527

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att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt	96
Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly	
20 25 30	
cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca	144
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro	
35 40 45	
gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc	192
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala	
50 55 60	
tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct	240
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser	

65	70								75								80								
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act																									288
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr																									
	85								90								95								
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc																									336
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu																									
	100								105								110								
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc																									384
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe																									
	115								120								125								
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt																									432
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly																									
	130								135								140								
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac																									480
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His																									
	145								150								155								160
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc																									528
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile																									
	165								170								175								
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc																									576
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser																									
	180								185								190								
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag																									624
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu																									
	195								200								205								
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc																									672
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly																									
	210								215								220								
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa																									720
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys																									
	225								230								235								240
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc																									768
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile																									
	245								250								255								
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac																									816
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp																									
	260								265								270								
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac																									864
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp																									
	275								280								285								
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc																									912
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val																									
	290								295								300								
aac gcg ctg tagctgtcaa tttaagaggc cag																									944
Asn Ala Leu																									
	305																								

<210> 528

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 528

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 20 25 30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
 35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
 50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser
 65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr
 85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu
 100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe
 115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly
 130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His
 145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile
 165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser
 180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu
 195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly
 210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys
 225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile
 245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp
 260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp
 275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val
 290 295 300

Asn Ala Leu
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 <213> Corynebacterium glutamicum

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 <223> RXA01360

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 Met Leu His Ile Ala
 1 5
 gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr
 10 15 20
 tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu
 25 30 35
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 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu
 40 45 50

<210> 530
 <211> 53
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 530
 Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly
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 20 25 30
 Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr
 35 40 45
 Thr Ser Ser Gly Glu
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<210> 531
 <211> 629
 <212> DNA
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<220>

<221> CDS

<222> (1)..(606)

<223> RXA01361

<400> 531

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acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg	96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu	
20 25 30	
gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg	144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala	
35 40 45	
aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc	192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg	
50 55 60	
gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt	240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe	
65 70 75 80	
gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc	288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu	
85 90 95	
gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc	336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly	
100 105 110	
gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att	384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile	
115 120 125	
gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc	432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr	
130 135 140	
ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg	480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala	
145 150 155 160	
tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca	528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala	
165 170 175	
cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt	576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu	
180 185 190	
gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga	626
Asp Val Cys Asp Pro Phe Arg His Gln Ile	
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tta	629

<210> 532

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 532

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Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
 20 25 30

Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
 35 40 45

Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
 50 55 60

Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
 65 70 75 80

Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
 85 90 95

Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
 100 105 110

Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
 115 120 125

Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
 130 135 140

Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
 145 150 155 160

Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
 165 170 175

Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
 180 185 190

Asp Val Cys Asp Pro Phe Arg His Gln Ile
 195 200

<210> 533

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA01208

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Leu	Asp	Ser	Leu	Thr 10	Leu	Val	Arg	Gln	Asn 15	Thr	Pro	Leu	Val	Gln 20	Cys	
ttg	acc	aac	tct	gtg	gtc	atg	caa	ttc	acg	gcc	aat	gtg	ttg	ctt	gcc	211
Leu	Thr	Asn	Ser 25	Val	Val	Met	Gln	Phe 30	Thr	Ala	Asn	Val	Leu 35	Leu	Ala	
gcg	ggt	gcg	acc	cct	gcg	atg	gtg	gat	act	cca	gct	gaa	tcg	gca	gaa	259
Ala	Gly	Ala 40	Thr	Pro	Ala	Met	Val 45	Asp	Thr	Pro	Ala	Glu 50	Ser	Ala	Glu	
ttc	gcc	gct	gtg	gcc	aat	gga	gtg	ctc	atc	aat	gcg	gga	act	cct	tct	307
Phe	Ala 55	Ala	Val	Ala	Asn	Gly 60	Val	Leu	Ile	Asn	Ala 65	Gly	Thr	Pro	Ser	
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Ala 70	Glu	Gln	Tyr	Gln	Gly 75	Met	Thr	Lys	Ala	Ile 80	Glu	Gly	Ala	Arg	Lys 85	
gct	ggc	aca	cca	tgg	gtg	tta	gac	cca	ggt	gct	gtg	ggt	ggg	ttg	tcg	403
Ala	Gly	Thr	Pro	Trp 90	Val	Leu	Asp	Pro	Val 95	Ala	Val	Gly	Gly	Leu 100	Ser	
gag	agg	acc	aag	tat	gcg	gag	gga	atc	gtc	gat	aag	cag	cct	gcc	gca	451
Glu	Arg	Thr	Lys 105	Tyr	Ala	Glu	Gly	Ile 110	Val	Asp	Lys	Gln	Pro 115	Ala	Ala	
att	cgt	gga	aac	gcc	tca	gag	gtc	gtg	gcg	ctt	gcg	ggg	ctc	ggt	gcc	499
Ile	Arg 120	Gly	Asn	Ala	Ser	Glu	Val 125	Val	Ala	Leu	Ala 130	Gly	Leu	Gly	Ala	
ggt	ggg	cgc	ggc	gta	gac	gcg	acc	gat	tcc	gtg	gaa	gtg	gcg	ttg	gag	547
Gly 135	Gly	Arg	Gly	Val	Asp	Ala 140	Thr	Asp	Ser	Val	Glu 145	Val	Ala	Leu	Glu	
gcg	gcg	caa	ttg	ttg	gcc	aag	cgc	act	ggt	ggc	gtc	gtg	gct	gtc	tct	595
Ala 150	Ala	Gln	Leu	Leu	Ala 155	Lys	Arg	Thr	Gly	Gly 160	Val	Val	Ala	Val	Ser 165	
ggt	gcg	gag	gac	ttg	att	gtg	tct	gcg	gat	cgg	gtg	acg	tgg	ttg	cgt	643
Gly	Ala	Glu	Asp 170	Leu	Ile	Val	Ser	Ala	Asp 175	Arg	Val	Thr	Trp 180	Leu	Arg	
tcg	ggg	gat	ccg	atg	ttg	cag	ctg	gtg	att	ggc	act	gga	tgc	tct	ttg	691
Ser	Gly	Asp	Pro 185	Met	Leu	Gln	Leu	Val 190	Ile	Gly	Thr	Gly	Cys 195	Ser	Leu	
ggc	gcg	ctg	aca	gct	gca	tat	cta	ggc	gcc	acg	ggt	gac	tca	gat	att	739
Gly	Ala 200	Leu	Thr	Ala	Ala	Tyr	Leu 205	Gly	Ala	Thr	Val	Asp 210	Ser	Asp	Ile	
tcc	gcg	cac	gat	gct	gtg	ttg	gct	gcg	cat	gcc	cat	gtg	ggt	gct	gct	787
Ser 215	Ala	His	Asp	Ala	Val	Leu 220	Ala	Ala	His	Ala	His 225	Val	Gly	Ala	Ala	
ggc	cag	att	gca	gca	cag	aag	gca	tcg	gcg	cca	ggc	agc	ttt	gcg	gtg	835
Gly	Gln	Ile	Ala	Ala	Gln	Lys	Ala	Ser	Ala	Pro	Gly	Ser	Phe	Ala	Val	

230 235 240 245
 gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg 883
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser
 250 255 260

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 Leu Val Asp Val Arg Glu Ala
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 <210> 534
 <211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 534
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 Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala
 20 25 30

 Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro
 35 40 45

 Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn
 50 55 60

 Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile
 65 70 75 80

 Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala
 85 90 95

 Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp
 100 105 110

 Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu
 115 120 125

 Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val
 130 135 140

 Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly
 145 150 155 160

 Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg
 165 170 175

 Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly
 180 185 190

 Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr
 195 200 205

 Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala
 210 215 220

 His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro
 225 230 235 240

Gly Ser Phe Ala Val Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala
245 250 255

Gln Ala Val Ala Ser Leu Val Asp Val Arg Glu Ala
260 265

<210> 535

<211> 1023

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

$\langle 222 \rangle$ (101) . . (1000)

<223> RXA00838

<400> 535

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tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115
Met Lys Ile Ala Ile
1 5

ggt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr
40 45 50

gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat 307
Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp
55 60 65

gta gtg atg att gct act aaa gca tta tgc cgg tct tta gat ctc gct 355
Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala

gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag 403
Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln
90 95 100

aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451
Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp
105 110 115

cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499
Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro
120 125 130

gcc tca gty tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp
135 140 145

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly
 150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys
 170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys
 185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu
 200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro
 215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu
 230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser
 250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val
 265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu
 280 285 290

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 Lys Glu Glu Glu Asn Ser Leu
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<210> 536

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 536

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 20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
 35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
 50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

65	70	75	80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val			
	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys			
	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe			
	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser			
	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr			
	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val			
	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly			
	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala			
	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala			
	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala			
	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala			
	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg			
	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr			
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Ala Gly Leu Lys Leu Lys Glu Glu Asn Ser Leu			
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 <222> (101)..(670)
 <223> RXA02400

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tttaagtcgc cagattaaag tcgtcaatga aaggacatac atg tct att tcc cgc 115
 Met Ser Ile Ser Arg
 1 5

acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163
 Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val
 10 15 20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211
 Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
 25 30 35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259
 Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser
 40 45 50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
 Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
 55 60 65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355
 Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr
 70 75 80 85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
 Phe Glu Thr Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
 90 95 100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451
 Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly
 105 110 115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
 Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
 120 125 130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
 Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
 135 140 145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
 Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
 150 155 160 165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
 Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
 170 175 180

gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac 690
 Glu Val Pro Val Thr Phe Ala Ala Ala
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tca 693

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<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 538

Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu
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<213> Corynebacterium glutamicum

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Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala			
55	60	65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag			355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu			
70	75	80	85
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa			403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln			
90	95	100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa			451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu			
105	110	115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt			499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly			
120	125	130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg			547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala			
135	140	145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag			595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu			
150	155	160	165
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga			643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly			
170	175	180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac			691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp			
185	190	195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct			739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala			
200	205	210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa			787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu			
215	220	225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat			835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn			
230	235	240	245
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca			883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr			
250	255	260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc			931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly			
265	270	275	
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac			979
Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His			
280	285	290	

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1027

Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
1075

Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
1123

Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
1171

Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
1219

Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
1267

Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
1315

Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
1363

Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
410 415 420

ggg gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
1411

Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
1459

Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
1507

Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
455 460 465

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1528

Ala Ala Gly Glu Ser Val Glu
470 475

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<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 540

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Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
 35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
 50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
 65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
 85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
 100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
 115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
 130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
 145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
 165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
 180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
 195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
 210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
 225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
 245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
 260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
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Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
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<210> 541

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> FRXA01209

<400> 541

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Met Cys Glu Arg Pro
1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	259
40 45 50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	307
55 60 65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	355
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	403
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	451
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	499
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	547
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag gcc atc gct gag Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	595
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	643
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	691
185 190 195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	739
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	787
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	835
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	883
250 255 260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	931
265 270 275	

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
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 455 460 465

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Ala Ala Gly Glu Ser Val Glu
470 475

<210> 542

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 542

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Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
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Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
 465 470 475

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(700)

<223> RXN01413

<400> 543

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 Leu Thr His Leu Phe
 1 5

tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163
 Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
 10 15 20

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
 Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
 25 30 35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
 Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
 40 45 50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
 Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Leu Pro Gln Ala Thr
 55 60 65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
 Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
 70 75 80 85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
 Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
 90 95 100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
 Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
 105 110 115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499
 Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
 120 125 130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
 Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
 135 140 145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
 Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
 150 155 160 165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
 Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
 170 175 180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
 Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
 185 190 195

gac aac aag tagagtttta aaataccgat caa 723
 Asp Asn Lys
 200

<210> 544

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 544

Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val
 1 5 10 15

Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
 20 25 30

Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg
 35 40 45

Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu
 50 55 60

Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr
 65 70 75 80

Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala
 85 90 95

Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly
 100 105 110

Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly
 115 120 125

Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val
 130 135 140

Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala
 145 150 155 160

Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val
 165 170 175

Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser
 180 185 190

Val Trp Leu Ala Glu Asp Asn Lys
 195 200

<210> 545
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(772)
 <223> BXN01617

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 tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115
 Leu Ile Leu Lys Thr
 1 5

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
 10 15 20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
 25 30 35

ggg atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu

40	45	50	
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc			307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys			
55	60	65	
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc			355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg			
70	75	80	85
gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag			403
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
90	95	100	
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
105	110	115	
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
120	125	130	
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
135	140	145	
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac			595
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
150	155	160	165
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
170	175	180	
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
185	190	195	
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
200	205	210	
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc			792
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
215	220		
cct			795

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<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 546

Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala
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Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu
 20 25 30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr
 35 40 45
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
 50 55 60
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr
 85 90 95
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu
 100 105 110
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly
 115 120 125
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn
 130 135 140
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu
 145 150 155 160
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala
 165 170 175
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala
 180 185 190
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val
 195 200 205
 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 210 215 220

<210> 547

<211> 638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(615)

<223> FRXA01617

<400> 547

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 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1 5 10 15
 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu

35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc			192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
50	55	60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac			240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac			288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
85	90	95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
100	105	110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
115	120	125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
130	135	140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
145	150	155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
165	170	175	
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
180	185	190	
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
195	200	205	
aaacaagctc cct			638

<210> 548

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 548

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Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
20 25 30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala

50	55	60
Leu Arg Ala Lys Val	Leu Pro Gln Ala Thr Val	Val Thr Pro Asn Asn
65	70	75 80
Phe Glu Ala Thr Thr	Leu Ser Gly Leu Asp Lys	Leu Glu Thr Ile Asp
	85	90 95
Asp Leu Lys Glu Ala Ala	Arg Leu Ile His Glu Gln Gly	Pro Gln Tyr
	100	105 110
Val Val Val Lys Gly Gly	Ile Asp Phe Pro Gly Asp	Asn Ala Val Asp
	115	120 125
Val Leu Phe Asp Gly Thr	Asp Tyr His Val Phe Ser	Glu Pro Lys Ile
	130	135 140
Gly Asp Glu Arg Val	Ser Gly Ala Gly Cys Thr	Phe Ala Ala Val Ile
	145	150 155 160
Thr Ala Glu Leu Ala	Lys Gly Asn Ser Ala Val	Asp Ala Val Thr Thr
	165	170 175
Ala Lys Arg Val Val	Thr Arg Ala Val Lys Asp	Ala Val Ala Ser Asn
	180	185 190
Ala Pro Phe Thr Ser	Val Trp Leu Ala Glu Asp	Asn Lys
	195	200 205

<210> 549

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> RXS01807

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	Met Pro Ser Ala Gly	
	1 5	
gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc		163
Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg		
	10 15 20	
gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg		211
Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly		
	25 30 35	
ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc		259
Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val		
	40 45 50	
gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct		307
Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser		

55	60	65	
cac cgc cag ccg atg tgc gac caa tgg ctc gcc gac gcg ctg caa gac			355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp			
70	75	80	85
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc			403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly			
90	95		100
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag			451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln			
105	110		115
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc			499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile			
120	125		130
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc			547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr			
135	140		145
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat			595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn			
150	155		160
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg			643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu			
170	175		180
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act			691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr			
185	190		195
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa			739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu			
200	205		210
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc			787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val			
215	220		225
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc			835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile			
230	235		240
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc			883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr			
250	255		260
aaa gcg ctt taggtttcgt ccgtctctga cag			915
Lys Ala Leu			

<210> 550

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

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Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
          20           25           30
Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
          35           40           45
Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
          50           55           60
Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
          65           70           75           80
Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
          85           90           95
Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
          100          105          110
Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
          115          120          125
Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
          130          135          140
Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
          145          150          155          160
Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
          165          170          175
Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
          180          185          190
Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
          195          200          205
Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
          210          215          220
Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
          225          230          235          240
Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
          245          250          255
Ala Gly Leu Gln Thr Lys Ala Leu
          260

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<210> 551
 <211> 622
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(622);
 <223> RXC01021

<400> 551

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 Met Ser Ser Ser Glu
 1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu
 10 15 20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211
 Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala
 25 30 35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259
 Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala
 40 45 50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307
 Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val
 55 60 65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355
 Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met
 70 75 80 85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403
 Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val
 90 95 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451
 Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg
 105 110 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499
 Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln
 120 125 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547
 Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu
 135 140 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595
 Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu
 150 155 160 165

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 170

<210> 552

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 552

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Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
 35 40 45

Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
 50 55 60

Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
 65 70 75 80

Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
 85 90 95

Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
 100 105 110

Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
 115 120 125

Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
 130 135 140

Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
 145 150 155 160

Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
 165 170

<210> 553
 <211> 1107
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1084)
 <223> RXN02246

<400> 553

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 Met Asp Val Ala His
 1 5

gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
 10 15 20

agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
 25 30 35

gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
 40 45 50

gtg gtc gcg ctt gca gct gcc gga gtc cgt gcc aac ggg ggc acg gcg	307
Val Val Ala Leu Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala	
55 60 65	
gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt	355
Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys	
70 75 80 85	
tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg ccg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg
310 315 320 325

aag gaa cac taaatgttca caggtattgt cga
1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
 210 215 220
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
 225 230 235 240
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
 245 250 255
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320
 Ile Glu Met Met Arg Lys Glu His
 325

<210> 555
 <211> 1107
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1084)
 <223> FRXA02246

<400> 555
 tgccgacgct ggcgtggatg ccttcgttgc aggttccgct gtgtacggcg ctgaggatcc 60
 caacaaggcg atccaggagt tgcgagcact cgcgacagtaa atg gat gtt gcg cac 115
 Met Asp Val Ala His
 1 5
 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
 10 15 20
 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
 25 30 35
 gtc gtt ggc gtt ggc gcc acg gca cct cct acg cgc cgc cac gcc gaa 259
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
 40 45 50
 gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307
 Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala
 55 60 65
 gtg gtc acc ctc gag ccg tgc aac cat tac gcc cgc acg ggt cca tgt 355
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	
aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc	1027
Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr	
295 300 305	
acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga	1075
Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg	

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga

1107

Lys Glu His

<210> 556

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
 1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
 20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
 35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
 50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
 65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
 85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
 100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
 115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
 130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
 145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
 165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
 180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
 195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
 210 215 220

Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
 225 230 235 240

Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
 245 250 255

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320
 Ile Glu Met Met Arg Lys Glu His
 325

<210> 557

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA02247

<400> 557

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ttcagatgta ttgatagaaa tgatgagaaa ggaacactaa atg ttc aca ggt att 115
 Met Phe Thr Gly Ile
 1 5

gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163
 Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser
 10 15 20

atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211
 Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu
 25 30 35

ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gta gca tcc ttt 259
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe
 40 45 50

ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307
 Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg
 55 60 65

agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg
 70 75 80 85

gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403
 Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His
 90 95 100

gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451
 Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp
 105 110 115

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val
120 125 130

gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser
135 140 145

ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg
150 155 160 165

gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu
170 175 180

gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val
185 190 195

gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733
Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp
200 205 210

taggttagac aacgtgagtg aac 756

<210> 558

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 558

Met Phe Thr Gly Ile Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu
1 5 10 15

His Leu Gly Asp Ser Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu
20 25 30

Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu
35 40 45

Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln
50 55 60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys
65 70 75 80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His
85 90 95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr
100 105 110

Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu
115 120 125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser
130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile
 145 150 155 160
 Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp
 165 170 175
 Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met
 180 185 190
 Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe
 195 200 205
 Thr Arg Asp
 210

<210> 559
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXN02248

<400> 559
 gatgtgatcg ctaagtacgt cgaacgcatg atgacgcgcg gcgtggctgg aaacactccc 60
 aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
 Val Ser Glu His Glu
 1 5
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
 10 15 20
 gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
 25 30 35
 gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
 40 45 50
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
 55 60 65
 gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
 70 75 80 85
 cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
 90 95 100
 ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu
 410 415 420

aac taaggagcac aacaatggct aaa
 1389
 Asn

<210> 560

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu
 1 5 10 15

Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp
 20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
 145 150 155 160
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
 165 170 175
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
 180 185 190
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
 195 200 205
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
 210 215 220
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
 225 230 235 240
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
 245 250 255
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
 420

<210> 561

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> FRXA02248

<400> 561

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gatgtgatcg ctaagtacgt cgaacgcatg atgacgcgcg gcgtggctgg aaacactccc 60

aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
                               Val Ser Glu His Glu
                               1           5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
                10                15                20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
                25                30                35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
                40                45                50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
                55                60                65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
                70                75                80                85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
                90                95                100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
                105                110                115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
                120                125                130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
                135                140                145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
                150                155                160                165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
                170                175                180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
                185                190                195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739

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Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171
 Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219
 Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267
 Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315
 Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363
 Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu

410

415

420

aac taaggagcac aacaatggct aaa
1389
Asn

<210> 562
<211> 422
<212> PRT
<213> Corynebacterium glutamicum

<400> 562
Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu
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Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp
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Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
35 40 45
Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
50 55 60
Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
65 70 75 80
Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
85 90 95
Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
100 105 110
His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
115 120 125
Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
130 135 140
Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
145 150 155 160

Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
165 170 175
Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
180 185 190
Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
195 200 205
Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
210 215 220
Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
225 230 235 240
Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
245 250 255

Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
 420

<210> 563
 <211> 600
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(577)
 <223> RXN02249

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 tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
 Met Ala Lys Glu Gly
 1 5
 ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20
 gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35
 gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259

Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
150 155

ttg 600

<210> 564

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly
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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> FRXA02249

<400> 565

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tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
 Met Ala Lys Glu Gly
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
 40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
 Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
 55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
 Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
 70 75 80 85

cca cac ttt gaa tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
 Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
 90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
 Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
 105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
 Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
 120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
 Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145
 gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
 Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 150 155

ttg 600

<210> 566
 <211> 159
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 566
 Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly
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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
 20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
 35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
 50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
 65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
 85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
 100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 567
 <211> 702
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(679)
 <223> RXA02250

<400> 567
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tgcgcgccac cgctaattag ttctaaggat ttgtgaaatc gtg aca acc aac gcc 115
 Val Thr Thr Asn Ala

	1	5	
ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc			163
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val	10	20	
ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc			211
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr	25	35	
gca gct ttc gct ggc acc acc aca acc aag cca tgg gag ctg gag gtg			259
Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro Trp Glu Leu Glu Val	40	50	
acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtg gtt gtc atc			307
Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile	55	65	
atg gcc gtt cac atc ttc atg ggt gcc gtg gtg gac gtc gat ttc acc			355
Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr	70	85	
ggt gca gcg gtc acc ttt gtt gac act ctg gca ttc cca gcg ttg ggc			403
Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly	90	100	
atc atc ttc tcc gtt ctt gtg ttc ttg gga ctg act cgc cct cgc gtg			451
Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val	105	115	
cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt			499
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg	120	130	
ttc tac cca tgg gtt gtc atc tac ggc atg tct ttc ccc aag ggc agc			547
Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser	135	145	
agc gtg gca cgt ttg gag ctt cca gac ttt gaa ttc gtt ccc atg tgg			595
Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu Phe Val Pro Met Trp	150	165	
gct ttc cag tcc cgc gat gga gaa gat gtg gtg cgc gcg gtt gcg acc			643
Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val Arg Ala Val Ala Thr	170	180	
ttc cgc gac ctc gaa aac aag tac atg cca gag gac taattaagct			689
Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu Asp	185	190	
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<210> 568

<211> 193

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

Val Thr Thr Asn Ala Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala

1 5 10 15

His	Ser	Gly	Ala	Val	Gly	Lys	Pro	Lys	Val	Gln	Leu	Ser	Asp	Ala	Glu	
			20				25						30			
Ile	Gln	Glu	Tyr	Thr	Ala	Ala	Phe	Ala	Gly	Thr	Thr	Thr	Thr	Lys	Pro	
			35				40						45			
Trp	Glu	Leu	Glu	Val	Thr	Thr	Lys	Phe	Leu	Lys	Lys	Ile	Ala	Trp	Val	
			50				55						60			
Ala	Val	Val	Val	Ile	Met	Ala	Val	His	Ile	Phe	Met	Gly	Ala	Val	Val	
			65				70						80			
Asp	Val	Asp	Phe	Thr	Gly	Ala	Ala	Val	Thr	Phe	Val	Asp	Thr	Leu	Ala	
			85						90						95	
Phe	Pro	Ala	Leu	Gly	Ile	Ile	Phe	Ser	Val	Leu	Val	Phe	Leu	Gly	Leu	
			100						105						110	
Thr	Arg	Pro	Arg	Val	Arg	Ala	Asn	Glu	Asp	Gly	Val	Glu	Val	Arg	Asn	
			115						120						125	
Phe	Ile	Gly	Thr	Arg	Phe	Tyr	Pro	Trp	Val	Val	Ile	Tyr	Gly	Met	Ser	
			130						135						140	
Phe	Pro	Lys	Gly	Ser	Ser	Val	Ala	Arg	Leu	Glu	Leu	Pro	Asp	Phe	Glu	
			145						150						155	
Phe	Val	Pro	Met	Trp	Ala	Phe	Gln	Ser	Arg	Asp	Gly	Glu	Asp	Val	Val	
			165						170						175	
Arg	Ala	Val	Ala	Thr	Phe	Arg	Asp	Leu	Glu	Asn	Lys	Tyr	Met	Pro	Glu	
			180						185						190	
Asp																

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<210> 569
<211> 1146
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1123)  
<223> RXA01489
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                                         Val Asp Ile Trp Ser
                                         1                     5
gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
                        10                      15                      20
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

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25	30	35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc			259
Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr			
40	45	50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc			307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr			
55	60	65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc			355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly			
70	75	80	85
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg			403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu			
90	95	100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg			451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala			
105	110	115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct			499
Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala			
120	125	130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat			547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn			
135	140	145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc			595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp Gln Arg Ile Cys Ser			
150	155	160	165
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac			643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn			
170	175	180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt			691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly			
185	190	195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac			739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr			
200	205	210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg			787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp			
215	220	225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat			835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp			
230	235	240	245
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc			883
Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser			
250	255	260	
gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca			931
Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala			
265	270	275	

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val
 280 285 290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac
 1027
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
 295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc
 1075
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
 310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct
 1123
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
 330 335 340

taaggccggt caccggccat caa
 1146

<210> 570

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 570

Val Asp Ile Trp Ser Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly
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Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln
 20 25 30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
 35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
 50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
 65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln
 130 135 140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu

165	170	175
Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly		
180	185	190
Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro		
195	200	205
Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly		
210	215	220
Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys		
225	230	235
Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr		
245	250	255
Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg		
260	265	270
Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly		
275	280	285
His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys		
290	295	300
Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr		
305	310	315
Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp		
325	330	335
Thr Gln Pro Ser Ala		
340		

<210> 571

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXA02135

<400> 571

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aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag	115
Met Val Pro Ala Glu	
1	5

ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg	163
Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr	
10	15
20	

aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag	211
Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys	
25	30
35	

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979

Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser
280 285 290

gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg
1027

Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met
295 300 305

tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag
1075

Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
310 315 320 325

att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc
1123

Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
330 335 340

gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg
1171

Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr
345 350 355

gag taactttcta agcgatgtcc ggc
1197
Glu

<210> 572

<211> 358

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 572

Met Val Pro Ala Glu Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys
1 5 10 15

Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
20 25 30

Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
35 40 45

Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
50 55 60

Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
65 70 75 80

Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
85 90 95

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
100 105 110

Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
115 120 125

Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala
 340 345 350
 Pro Glu Gln Asn Thr Glu
 355

<210> 573
 <211> 1146
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1123)
 <223> RXA01489

<400> 573
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 agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115
 Val Asp Ile Trp Ser
 1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att	163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile	
10 15 20	
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag	211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu	
25 30 35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc	259
Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr	
40 45 50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc	307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr	
55 60 65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	
70 75 80 85	
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg	403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu	
90 95 100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg	451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala	
105 110 115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct	499
Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala	
120 125 130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat	547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn	
135 140 145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc	595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Gln Arg Ile Cys Ser	
150 155 160 165	
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac	643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn	
170 175 180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt	691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly	
185 190 195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	
200 205 210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	
215 220 225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp	
230 235 240 245	
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc	883

Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser
 250 255 260

gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca 931
 Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala
 265 270 275

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val
 280 285 290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac
 1027

Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
 295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc
 1075

Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
 310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct
 1123

Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
 330 335 340

taaggccggt caccggccat caa
 1146

<210> 574
 <211> 341
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 574
 Val Asp Ile Trp Ser Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly
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Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln
 20 25 30

Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
 35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
 50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
 65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln

130 135 140
 Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160
 Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu
 165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
 305 310 315 320
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
 325 330 335
 Thr Gln Pro Ser Ala
 340

<210> 575
 <211> 805
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (87)..(782)
 <223> RXN01712

<400> 575
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 Met Val Asp Ile Leu Glu Leu Ile Gly
 1 5

ccc cta cct ttt gtg tct acg cca gag tta agg gca att gtc gtg act 161
 Pro Leu Pro Phe Val Ser Thr Pro Glu Leu Arg Ala Ile Val Val Thr

10	15	20	25	
gcc att aat ggt tcc acc act att aat ggc acg tct ggt cag ctt gga				209
Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly				
	30	35	40	
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac				257
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp				
	45	50	55	
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc				305
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly				
	60	65	70	
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag				353
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln				
	75	80	85	
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat				401
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp				
	90	95	100	105
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc				449
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile				
	110	115	120	
acg gat aat tcc gat caa gca aag cag cag cgg ctt gtg gat gct ggg				497
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly				
	125	130	135	
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa				545
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu				
	140	145	150	
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca				593
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala				
	155	160	165	
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat				641
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His				
	170	175	180	185
cag acg att gat ccg acg ttg tag ggc agc gtc gag ggc ggc ggc ggc				689
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val				
	190	195	200	
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt				737
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe				
	205	210	215	
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag				782
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys				
	220	225	230	
tgagtgttgg actctccgga tct				805

<210> 576

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

Met Val Asp Ile Leu Glu Leu Ile Gly Pro Leu Pro Phe Val Ser Thr
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Pro Glu Leu Arg Ala Ile Val Val Thr Ala Ile Asn Gly Ser Thr Thr
 20 25 30

Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu
 35 40 45

Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser
 50 55 60

Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile
 65 70 75 80

Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala
 85 90 95

Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu
 100 105 110

Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala
 115 120 125

Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu
 130 135 140

Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr
 145 150 155 160

Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu
 165 170 175

Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu
 180 185 190

Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro
 195 200 205

Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu
 210 215 220

Phe Leu Arg Tyr Lys Arg Ala Lys
 225 230

<210> 577

<211> 578

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (55)..(555)

<223> FRXA01712

<400> 577

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 Val

1

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aag gct gaa aat tat ggt ggc gtg gag gtt tcg cct gaa atc cag aag 105
Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys
      5              10              15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met
      20              25              30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala
      35              40              45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln
      50              55              60              65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu
      70              75              80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg
      85              90              95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala
      100             105             110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly
      115             120             125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg
      130             135             140             145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537
Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe Leu
      150             155             160

ccg tat aag cgc gcc aag tga gtt ttg act ttc cga tct 578
Arg Tyr Lys Arg Ala Lys
      165

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<210> 578

<211> 167

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 578

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Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln
  1              5              10              15

Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val
      20              25              30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu
      35              40              45

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Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys
50 55 60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr
65 70 75 80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala
85 90 95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala
100 105 110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser
115 120 125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg
130 135 140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe
145 150 155 160

Leu Arg Tyr Lys Arg Ala Lys
165

<210> 579

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> RXN02384

<400> 579

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aatacgagcc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115
Val Thr Arg Arg Leu
1 5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163
Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met
10 15 20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211
Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala
25 30 35

gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259
Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe
40 45 50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307
Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala
55 60 65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355
Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr				
	90	95	100	
cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro				
	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val				
	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu				
	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu				
	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr				
	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu				
	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro				
	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly				
	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaaa atg				831
Trp Asn Met Gly Val Thr Gln				
	230	235		

<210> 580

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

Val	Thr	Arg	Arg	Leu	Ile	Leu	Leu	Arg	His	Gly	Gln	Thr	Glu	Tyr	Asn
1				5				10					15		

Ala	Thr	Ser	Arg	Met	Gln	Gly	Gln	Leu	Asp	Thr	Glu	Leu	Ser	Asp	Leu
			20					25					30		

Gly	Phe	Gln	Gln	Ala	Ala	Ser	Ala	Ala	Ser	Val	Leu	Val	Gln	Lys	Asn
		35					40						45		

Ile	Thr	His	Val	Phe	Ser	Ser	Asp	Leu	Ser	Arg	Ala	Phe	Asn	Thr	Ala
	50						55				60				

Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg
 65 70 75 80

Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu
 85 90 95

Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro
 100 105 110

Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg
 115 120 125

Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp
 130 135 140

Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu
 145 150 155 160

Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser
 165 170 175

Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr
 180 185 190

Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala
 195 200 205

Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln
 210 215 220

Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln
 225 230 235

<210> 581

<211> 453

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXN01560

<400> 581

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tgcatcagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac 115
 Val Gly Val Ser Tyr
 1 5

atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 165
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
 10 15 20

att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
 25 30 35

acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

40	45	50	
atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg			307
Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu			
55	60	65	
ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca			355
Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser			
70	75	80	85
ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac			403
Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr			
90	95	100	
ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc			450
Gly Val Asn Gly Pro Val Asp Ala Asn			
105	110		
ttt			453

<210> 582
 <211> 110
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 582
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 Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
 20 25 30
 Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
 35 40 45
 Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
 50 55 60
 His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
 65 70 75 80
 Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
 85 90 95

Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
 100 105 110

<210> 583
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXN00667

<400> 583
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															Met	Ile	Ala	Leu	Lys	5
tcc	atg	tct	aac	agg	gta	gta	caa	aag	cca	aaa	atg	aaa	gcg	ccg	cta					163
Ser	Met	Ser	Asn	Arg	Val	Val	Gln	Lys	Pro	Lys	Met	Lys	Ala	Pro	Leu					20
				10					15											
ccc	atc	cgc	gac	ggc	ctc	aac	cct	tcc	cgt	gtg	cgc	ttg	ccg	ctc	gac					211
Pro	Ile	Arg	Asp	Gly	Leu	Asn	Pro	Ser	Arg	Val	Arg	Leu	Pro	Leu	Asp					
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gcg	gcg	ccg	atc	cgc	gcc	atc	gat	ttt	gtt	gaa	tac	ctc	att	tcc	acg					259
Ala	Ala	Pro	Ile	Arg	Ala	Ile	Asp	Phe	Val	Glu	Tyr	Leu	Ile	Ser	Thr					
		40					45					50								
cag	cgc	cac	cgc	aat	ccg	gcc	gac	aac	gcc	gaa	gcg	ctt	caa	gcg	cgt					307
Gln	Arg	His	Arg	Asn	Pro	Ala	Asp	Asn	Ala	Glu	Ala	Leu	Gln	Ala	Arg					
	55					60					65									
ttc	gac	gcc	gac	ctt	gtt	gtc	aac	cac	tac	ggc	gag	ccc	tac	gcc	ccc					355
Phe	Asp	Ala	Asp	Leu	Val	Val	Asn	His	Tyr	Gly	Glu	Pro	Tyr	Ala	Pro					85
	70				75					80										
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Asp	Thr	Met	Val	Gln	Pro	Asp	Asp	Asp	Ile	Trp	Phe	Tyr	Arg	Met	Pro					
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gcc	gcc	gaa	cgg	ccg	atc	cct	tac	aaa	att	cat	gtc	att	cac	gaa	gac					451
Ala	Ala	Glu	Arg	Pro	Ile	Pro	Tyr	Lys	Ile	His	Val	Ile	His	Glu	Asp					
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Asp	Asp	Ile	Leu	Val	Ile	Asp	Lys	Pro	Pro	Tyr	Leu	Ala	Thr	Met	Pro					
		120					125					130								
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Arg	Gly	Arg	His	Ile	Thr	Glu	Thr	Ala	Leu	Val	Lys	Met	Arg	Val	Leu					
	135					140					145									
act	gga	aac	aac	gat	ctc	acc	cca	gct	cac	cgc	ctc	gat	cgc	ctg	act					595
Thr	Gly	Asn	Asn	Asp	Leu	Thr	Pro	Ala	His	Arg	Leu	Asp	Arg	Leu	Thr					
	150				155					160				165						
tcc	ggt	gtg	tta	gtc	atg	gtg	aaa	aaa	cca	gaa	ctc	cgt	ggc	gct	tac					643
Ser	Gly	Val	Leu	Val	Met	Val	Lys	Lys	Pro	Glu	Leu	Arg	Gly	Ala	Tyr					

ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu
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gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg
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caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu
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cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu
 280 285 290

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 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met
 295 300 305

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 1075
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu
 310 315 320 325

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 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His
 100 105 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr
 115 120 125
 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val
 130 135 140
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg
 145 150 155 160
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu
 165 170 175
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys
 180 185 190
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly
 195 200 205
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln
 210 215 220
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser
 225 230 235 240
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His
 245 250 255
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly
 260 265 270
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile
 275 280 285
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp
 290 295 300
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Ser Leu

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832

230 235 240 245
 gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca 883
 Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro
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 tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc 931
 Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe
 265 270 275
 ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct 979
 Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro
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 Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val
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 gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc
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 Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser
 310 315 320 325
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 Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr
 330 335 340
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 Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile
 345 350 355
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 Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile
 360 365 370
 acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt
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35	40	45
Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr 50 55 60		
Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu 65 70 75 80		
Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp 85 90 95		
Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu 100 105 110		
Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile 115 120 125		
Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys 130 135 140		
Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro 145 150 155 160		
Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly 165 170 175		
Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala 180 185 190		
Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro 195 200 205		
Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu 210 215 220		
Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu 225 230 235 240		
Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe 245 250 255		
Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu 260 265 270		
Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser 275 280 285		
Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val 290 295 300		
Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro 305 310 315 320		
Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu 325 330 335		
Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe 340 345 350		
Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr 355 360 365		

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Thr Ala
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 <223> RXC02380

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 Met Thr Thr Thr Val
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 aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
 10 15 20
 cat aat ggt cac ctt gtg cgc ggc tca gag gta gcg gat cga ttc gat 211
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
 25 30 35
 ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
 40 45 50
 aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
 55 60 65
 gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
 70 75 80 85
 cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
 90 95 100
 caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
 105 110 115
 gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
 120 125 130
 cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
 135 140 145

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
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 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
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<210> 588

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
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Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

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Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys
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Met Thr Thr Thr Val
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aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
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His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
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Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
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Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
105 110 115

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Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
120 125 130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
135 140 145

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 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
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 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
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 Gly Gln Asn Gln Ala
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<210> 590

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

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Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
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Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val
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 Val Ser Ala Leu Glu
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 Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
 10 15 20

aag gcc gat gac atc gct gtc atc gat gtc tct gac atg atc gca atc 211
 Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
 25 30 35

acc gat tgc ttt gtt gtt gca tct gct gac aat gag cgc cag gtg ggc 259
 Thr Asp Cys Phe Val Val Ala Ser Ala Asp Asn Glu Arg Gln Val Gly
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 Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
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 Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
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 Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu
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 Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp
 120 125 130

atc cgc aac atc gac agc att gat gaa ctc cca cct ttg cca gct gaa 547
 Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu

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 Glu Arg Gln Val Gly Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr
 50 55 60
 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
 65 70 75 80
 Trp Val Leu Leu Asp Tyr Gly Leu Val Val Ile His Val Gln Arg Gln
 85 90 95
 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
 100 105 110
 Leu Ile Glu Ile Glu Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp
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 Val Leu Gly Ala Val
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Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp	
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Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val	
25 30 35	
acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg	259
Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu	
40 45 50	
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Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met	
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Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly	
70 75 80 85	
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Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys	
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ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg	451
Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val	
105 110 115	
ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag	499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
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Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
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ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
170 175 180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt	883

Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu
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 cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg 931
 Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val
 265 270 275
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 Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr
 280 285 290
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 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser
 295 300 305
 ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg
 1075
 Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu
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 cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc
 1123
 Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile
 330 335 340
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 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
 345 350 355
 ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac
 1219
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
 360 365 370
 ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc
 1267
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385
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 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
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 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
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 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
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atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc
1507

Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt
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Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
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1603

Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
490 495 500

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1651

Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
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1699

Pro Val Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
520 525 530

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1747

Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
535 540 545

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1795

His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
550 555 560 565

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1843

Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag
1891

Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta
1939

Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg
1987

Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt
2035

Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc
2083

Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag
2131

Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
665 670 675

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2179

Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
680 685 690

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2227

Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
695 700 705

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2275

Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
710 715 720 725

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2323

Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc
2371

Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct
2419

Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg
2467

~~Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met~~
775 780 785

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2515

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790 795 800 805

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2563

Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct
2611

Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
825 830 835

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2659

Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
840 845 850

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Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
855 860 865

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Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
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acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc
2803

Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
890 895 900

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2851

Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
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2899

Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
920 925 930

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2947

Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
935 940 945

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2995

Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
950 955 960 965

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3043

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Val Gly Trp

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<211> 984

<212> PRT

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<400> 594

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Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu